us-09-445-576a-38.rai

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08 452-592B-8
US-08 452-592B-9
US-08 452-592B-1
US-08 452-592B-1
US-08 956-20
US-08 956-20
US-08 950-571-20
US-08 990-571-49
US-08 723-142A-20
US-08 723-142A-20
US-09 52B-784A-49
US-09 52B-784A-49
US-09 52B-784A-49
US-09 55B-784A-49
US-09 55B-784A-49
US-09 55B-784A-49
US-09 55B-784A-49
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US-08 55B-784A-49
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US-08 55B-784A-49
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US-07-745-206A-2
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                               protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Logical Steven G.
APPLICANT: Mu, Jiangen G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER FILE REPERENCE: 210121.446C5
CURRENT APPLICATION NUMBER: US/09/602,877A
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 56, Application US/08469486
Patent No. 5739281
GENERAL INFORMATION:
APPLICANT: Thosersen, Hans Christian
APPLICANT: Holtet, Thor Las
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of
TITLE OF INVENTION: proteins
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             jo
                                         US-09-304-121-2
US-09-513-783A-176
US-09-513-783A-176
US-09-178-4778-2
US-09-178-4778-2
US-09-178-4778-2
US-09-171-035-484
US-09-134-001C-5178
US-08-956-3078-1
US-08-973-462-8
US-08-973-462-8
US-08-973-462-8
US-08-973-462-8
US-08-713-815A-4
US-08-713-815A-3
US-08-713-815A-3
US-09-610-401-3
US-08-718-815A-3
US-08-718-815A-3
US-08-718-815A-3
US-08-718-815A-3
US-09-610-401-3
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Pred. No. 5.9e-15;
; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 99, Application US/09602877A ; Patent No. 6432707
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ilarity 86.1%;
Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-09-602-877A-99
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Best Local Similarity
Matches 31; Conserv
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CITY: Boston
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LENGTH: 197
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Sequence 8, Application US/08452592B
Patent No. 5712366
GENERAL INFORMATION:
APPLICANT: Kaplan, David L.
TITLE OF INVENTION: Fabrication of Nanoscale Materials Using
TITLE OF INVENTION: Self-Assembling Proteins
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                         ; DB 2; Length 202; 0.0027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 84;
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MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage COMPUTER: TBM PC Compatable COMPUTER: TBM PC COMPATABLE CORPATING SYTEM: DOS 6.22 SOFTWARE: WORDPERFECT Version 6.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,592B
FILING DATE: 25 May 1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: U.S. Army Soldier Systems Command AMSCC-CC (Patent Counsel)
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Pred. No. 0.19;
5; Mismatches
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STATE: Massachsuetts
COUNTRY: United States of America
ZIP: 01760-5035
                                                                                                                                                                                                                                                                                                                                                             9 DLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,948
FILING DATE: 25 May 1993
ATTONEY/AGENT INFORMATION:
NAME: Donahue, Richard J.
NAME: Lamming, John H.
NAME: Ranucci, Vincent J.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FELECOMMUNICATION INFORMATION TELEPHONE: 508-233-4510
                 TELEPHONE: 617 542 5070
TELEFAR: 617 542 8906
TELEA: 200154
INFORMATION FOR SEQ ID NO: 56
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TYPE: amino acids
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Matches 16, Conservative
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MOLECULE TYPE: protein
US-08-469-658-56
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ADDRESSEE: U.S. Army
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REGISTRATION NUMBER:
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Best Local Similarity
Matches 14; Conserv
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US-08-452-592B-8
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APPLICANT: Holtet, Thor Las
APPLICANT: Holtet, Thor Las
APPLICANT: Etzect, Michael
TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 79; DB 1; Le
Pred. No. 0.0027;
7; Mismatches 5;
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ZIP: 0210-2804
ZIP: 0210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: BAT PC Compatible
COMPUTER: BAT PC Compatible
COMPUTER: BAT PC Compatible
COMPUTER: BAT PC COMPACE
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
TI.ING DATE: June 5, 1995
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002001
TELECOMMUNICATION INFORMATION:
TELEPAX: 617 542 8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 ELKSRLDTLAQEVALLKEQQALQTVCLK 73
                                         SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 56, Application US/08469658 Patent No. 5917018 GENERAL INFORMATION:
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APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
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nilarity 57.1%;
Conservative 7
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NAME: Paul T. Clark
REGISTRATION NUMBER: 30,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-469-486-56
                                                                                                                                                   CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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Best Local Similarity
Matches 16; Conserv
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Patent No. 5712366
GENERAL INFORMATION:
APPLICANT: MCGTAth, Kevin P.
APPLICANT: Kaplan, David L.
TITLE OF INVENTION: Fabrication of Nanoscale Materials Using TITLE OF INVENTION: Self-Assembling Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.7%; Score 58; DB 1; Length 84; 48.1%; Pred. No. 0.64;
                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage COMPUTER: IBM PC Compatable COMPUTER: IBM PC COMPATABLE COMPUTER: IBM PC COMPATABLE COMPATAIN SYSTEM: WordPerfect Version 6.1 SOFTWARE: WordPerfect Version 6.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,592B FILING DATE: 25 May 1995
FILING DATE: 25 May 1995
FILING DATE: 25 May 1993
ATTORNEY/AGENT INFORMATION:
NAME: Lonablue, Richard J.
NAME: Lonablue, Richard J.
NAME: Ranucci, Vincent J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachsuetts
COUNTRY: United States of America
ZIP: 01760-5035
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
COMPUTER: IBM PC Compatable
OPERATING SYSTEM: DOS 6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: U.S. Army Soldier Systems Command
STREET: AMSCC-CC (Patent Counsel)
CITY: Natick
STATE: Massachsuetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 22,062 (Donahue)
REGISTRATION NUMBER: 34,857 (Lamming)
REGISTRATION NUMBER: 29,579 (Ranucci)
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CLASSIFICATION: 530
RIOR ADDITOR: 530
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,592B
  AMSCC-CC (Patent Counsel)
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APPLICATION NUMBER: 08/068,948
FILING DATE: 25 May 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 508-233-4510
                                             STATE: Massachsuetts
COUNTRY: United States of
ZIP: 01760-5035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
Matches 13; Conserva
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US-08-452-592B-10
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                                                                                                                                                                                                                            APPLICANT: McGrath, Kevin P.
APPLICANT: Kaplan, David L.
TITLE OF INVENTION: Fabrication of Nanoscale Materials Using
TITLE OF INVENTION: Self-Assembling Proteins
CORRESPONDENCE: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: McGrath, Kevin P.
APPLICANT: Kaplan, David L.
TITLE OF INVENTION: Fabrication of Nanoscale Materials Using TITLE OF INVENTION: Self-Assembling Proteins NUMBER OF SEQUENCE: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 84;
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                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Natick
STATE: Massachsuetts
COUNTRY: United States of America
ZIP: 01760-25035
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: U.S. Army Soldier Systems Command STREET: AMSCC-CC (Patent Counsel)
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REGISTRATION NUMBER: 34,857 (Lamming)
REGISTRATION NUMBER: 29,579 (Ranucci)
REFERENCE/DOCKET NUMBER: NA-1096D
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatable
OPERATING SYSTEM: DOS 6.22
SOFTWARE: WordPerfect Version 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,592B
FILING DATE: 25 May 1995
CLASSIFICATION: 530
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3 VKEKDGDLKTQVEKLWREVNALKEMQA 29
                       3 VKEKDGDLKTQVEKLWREVNALKEMQA 29
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,948
FILING DATE: 25 May 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                      Sequence 9, Application US/08452592B Patent No. 5712366 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08452592B Patent No. 5712366
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Ranucci, Vincent J.
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LENGTH: 84 amino acids
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Best Local Similarity
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US-08-452-592B-7
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                                                                                                                                                                                                                             APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 367;
       Indels
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STREET: 6300 COlumbia Center, 701 Fifth Avenue CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
     6
     Mismatches
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Pred. No.
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                                                              4 KEKDGDLKTQVEKLWREVNALKEMQA 29
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     2
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Mak1, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/FOCKET NUMBER: 21
TELECOMMUNICATION: INFORMATION:
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36.0%;
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TELEFAX: (206)682-6031
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-APR-1997
   12; Conservative
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Best Local Similarity 36.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
FILING DATE: 24-APR
CLASSIFICATION: 435
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US-08-845-258-20
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US-08-845-258-49
     Matches
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                                                                                                                                                                                                                                                                                                                                                                               8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
OSTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/08956307B
Patent No. 6090911
GENERAL INFORMATION:
APPLICANT: Tirrell, David A.
APPLICANT: Tirrell, David A.
APPLICANT: Kevin P. McGrath
TITLE OF INVENTION: REVERSIBLE HYDROGELS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          Score 54; DB
Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                      Query Match 29.5%; Score 54; DB Best Local Similarity 44.4%; Pred. No. 2.2; Matches 12; Conservative 7; Mismatches
                                                    NAME: Ranuccí, Vincent J.
REGISCYRATION NUMBER: 22,062 (Donahue)
REGISTRATION NUMBER: 32,679 (Lamming)
REGISTRATION NUMBER: 29,579 (Ranucci)
REFERENCE/POCKET NUMBER: Na-1096D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-233-4510
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION NUMBER:
RAPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                      39 LKAKIGDLENEVAQLEREVRSLEDEAA 65
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REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 18:
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                     Donahue, Richard J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                            LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
TYPE: amino acid
                                   Lamming, John H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 617/542-8906
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02110-2804
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Best Local Similarity
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COUNTRY:
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Sequence 49, Application US/08990571
Patent No. 6214971
GENERAL INFORMATION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF INTERPREDIATE OF SEQUENCES: 79
CORRESPONDENCE ADDRESS: ADDRESSE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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APPLICANT: Rodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Faul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 49
                                                                             Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 367;
                                                                                                                  Indels
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                                                                             DB 4;
22;
                                                                           Query Match 28.4%; Score 52; DB Best Local Similarity 36.0%; Pred. No. 22; Matches 9; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 11-DEC-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 20, Application US/08723142A
; Patent No. 6306396
                                                                                                                                                                               :::|||| | |::|:|: |
280 KITKKDGDYNTHFEDMIKELNSAAE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 KITKKDGDYNTHFEDMIKELNSAAE 304
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                                                                                                                                                        2 RVKEKDGDLKTQVEKLWREVNALKE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 622-4900
TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 499
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.4%;
Best Local Similarity 36.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 367 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 Colum
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
    STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-723-142A-20
                      ; TOPOLOGY:
US-08-990-571-20
                                                                                                                                                                                                                                                                           US-08-990-571-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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                                                                                                                                                                                                                                                          RESULT 12
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Patent No. 6214971
GENERAL INFORMATION:
APPLICANT: Reed, Steven G. et al.
TILLE OF INVENTION:
COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B.
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/990,571
FILING DATE: 11-DEC-1997
                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52; DB 4; Pred. No. 22; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/POCKET NUMBER: 210121.426C2
TELECOMMUNICATION INFORMATION:
TELEPENX: (206) 622-4900
TELEPENX: (206) 682-6931
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                    210121.426C1
                                                                                                                                                                                   24-APR-1997
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280 KITKKDGDYNTHFEDMIKELNSAAE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RVKEKDGDLKTQVEKLWREVNALKE 26
                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGIGSRATION NUMBER: 31,392
REFRENCE/CDCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.4%;
36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                  Seattle
: Washington
XY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98104
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                                                         COUNTRY:
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Gaps

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GENERAL INFORMATION:
APPLICANT: Reced, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Hodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Bleath, Paul R.
APPLICANT: McWeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C4
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO. 20
LENGTH: 367
TYPE: PRT
CREATER PRT
CREATER BABDESIA MICROTI
                                                                                                                                                                                                                              28.4%; Score 52; DB 4; Length 367; 36.0%; Pred. No. 22; Live 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.4%; Score 52; DB 4; Length 367; 36.0%; Pred. No. 22; tive 7; Mismatches 9; Indels
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Job time : 11 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 20, Application US/09528784A ; Patent No. 6451315
                                                                                                                                                                                                                                                                                                                                                  280 KITKKDGDYNTHFEDMIKELNSAAE 304
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                       TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 49
SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                            Query Match
Best Local Similarity 36.0°
Matches 9; Conservative
                                                                                                                                    sss: single
linear
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Best Local Similarity
Lase 9; Conservat
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US-08-723-142A-49
           TELEPHONE:
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US-09-528-784A-20
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghon, Raymond
APPLICANT: Hought, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 367;
                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPTUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURFENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,142A
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J
REGISTRATION NUMBER: 210121.426
FELEPHONE: (206) 682-693
FELEPHONE: (206) 682-693
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
LENGTH: 367 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/723,142A
FILING DATE: 01-OCT-1996
FILING DATE: 536
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seathle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 22;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426
TELEÇOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 49, Application US/08723142A Patent No. 6306396 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 KITKKDGDYNTHFEDMIKELNSAAE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 RVKEKDGDLKTQVEKLWREVNALKE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 28.4%;
Best Local Similarity 36.0%;
Matches 9; Conservative 7
                                                                CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-723-142A-20
                                                                                                                 USA
                                                                                                                                 98104
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                                                                                                                 COUNTRY:
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us-09-445-576a-38.rapb

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April 15, 2003, 11:50:25 ; Search time 10 Seconds (without alignments) 220.090 Million cell updates/sec
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                        US-09-445-576A-38
183
1 RRVKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                            248812 seqs, 61136040 residues
                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                          Run on:
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/cgn2_6/ptodata/2/pubpaa/RCT_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* Published_Applications_AA:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

- Description	Sequence 41, Appl		. ~	403,	Sequence 403, App				Sequence 403, App	403,	Sequence 403, App	Sequence 403, App	Sequence 2, Appli	Sequence 403, App	Sequence 276, App	Sequence 276, App	276,	403,	276.
ΩI	US-09-987-107-41	US-09-745-288-99	US-09-938-418-10	US-09-992-598-403	US-09-989-293A-403	US-09-989-735-403	US-09-990-444-403	US-09-989-730-403	US-09-990-436-403	US-09-991-181-403	US-09-993-687-403	US-09-989-734-403	US-10-127-966-2	US-09-997-653-403	US-10-174-590-276	US-10-176-758-276	US-10-175-737-276	US-09-993-667-403	US-10-173-706-276
DB	6	10	σ	σ	9	6	9	9	6	6	6	6	σ	6	6	6	σ	6	0
% Query Match Length DB	36	197	206	206	206	206	206	206	206	206	206	206	206	206	206	206	206	206	206
% Query Match	100.0	7.06	90.7	90.7	90.7	7.06	90.7	90.7	90.7	7.06	90.7	90.7	7.06	20.7	90.7	7.06	90.7	90.7	90.7
Score	183	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166	166
Result No.	н	7	ო	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19

Sequence 276, App Sequence 403, App Sequence 276, App Sequence 276	
US-10-175-738-276 US-10-175-738-276 US-10-175-722-276 US-10-176-913-276 US-10-180-552-276 US-10-180-552-276 US-09-990-438-403 US-09-990-438-403 US-09-990-438-403 US-09-990-666-403 US-09-997-666-403 US-10-173-700-276 US-10-174-572-276 US-10-174-582-276 US-10-175-739-276 US-10-175-739-276 US-10-175-743-276 US-10-175-743-276 US-10-175-743-276 US-10-176-498-276 US-10-176-498-276 US-10-176-498-276 US-10-176-498-276 US-10-176-498-276 US-10-176-498-276 US-10-176-498-276 US-10-176-498-276 US-10-176-498-276 US-10-176-998-276 US-10-176-998-276 US-10-176-998-276 US-10-176-998-276 US-10-176-998-276 US-10-176-998-276 US-10-176-998-276 US-10-176-998-276	
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                                                                                                                                            APPLICANT: MOESTRUP, Soren
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
PRIOR PILIAG DATE: 2001-01-15
PRIOR PLICATION NUMBER: US 60/264,022
PRIOR PILIAG DATE: 2001-01-15
PRIOR PLICATION NUMBER: DK PA2001 00057
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RRVKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
                                               Sequence 41, Application US/09987107
Patent No. US200210560741
GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Box taurus
RESULT 1
US-09-987-107-41
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LENGTH: 36
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; Sequence 99, Application US/09745288; Patent No. US20010018058A1; GENERAL INFORMATION: RESULT 2 US-09-745-288-99 QQ

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APPLICANT: Reed, Steven G. APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C.

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Gaps

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Length 206; Indels

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITTLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C20
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Pred. No. 3.6e-14;
4; Mismatches 1
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CURRENT PEDLICATION NUMBER: 05/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR PEDLICATION NUMBER: 06/049787
PRIOR FILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR PILING DATE: 1997-11-24
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1998-02-25
PRIOR PELING DATE: 1998-02-25
                                                         PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-06-20
PRIOR FILING DATE: 2001-06-29
PRIOR PLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
      PCT/US01/06520
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Patent No. US20020160384A1
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Williams, P. Mickey
Wood, William I.
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86.1%;
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Goddard, Audrey
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Kljavin, Ivar J.
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Best Local Similarity 86.1
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumas, Danie
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                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 10
LENGTH: 206
TYPE: PRT
ORGANISM: Homo Sapien
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US-09-992-598-403
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COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                     Length 197;
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                                                     FILE REFERENCE: 210121.44601
CURRENT APPLICATION NUMBER: US/09/745,288
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                  90.7%; Score 166;
86.1%; Pred. No. 3
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CURRENT APPLICATION NUMBER: US/09/938,418
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 60/081,071
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APPLICATION NUMBER: PCT/US99/12252
TLING DATE: 1999-06-02
APPLICATION NUMBER: PCT/US99/20111
FILING DATE: 1999-09-01
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PPILCATION NUMBER: PCT/US00/23328
FILING DATE: 2000-08-24
APPLICATION NUMBER: PCT/US00/32678
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APPLICATION NUMBER: PCT/US99/05028
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APPLICATION NUMBER: PCT/US00/04342
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APPLICATION NUMBER: PCT/US00/08439
FILING DATE: 2000-03-30
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APPLICATION NUMBER: PCT/US00/04341
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APPLICATION NUMBER: PCT/US00/05841
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R APPLICATION NUMBER: 60/097,022
R FILING DATE: 1998-08-18
R APPLICATION NUMBER: 60/101,922
R FILING DATE: 1998-09-24
R APPLICATION NUMBER: 60/103,679
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APPLICATION NUMBER: 60/085,697
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                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 86.1
Matches 31; Conservative
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                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapien
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                LENGTH: 197
                                                                                                                                                                                 SOFTWARE: F
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1998-03-20 NUMBER: 60/083322 1998-04-28 NUMBER: 60/084600 1998-05-07 NUMBER: 60/087106 1998-05-08 NUMBER: 60/087609 1998-06-02 NUMBER: 60/08759 1998-06-02 NUMBER: 60/08759 1998-06-02 NUMBER: 60/08759	1998-06-04 NUMBER: 60/0880 1998-06-04 NUMBER: 60/0880 1998-06-04 NUMBER: 60/0880 1998-06-04 NUMBER: 60/0881 1998-06-04 NUMBER: 60/0882 NUMBER: 60/0887 NUMBER: 60/0888	BER: 98-0-0 98-0-0 98-0-0 98-0-0 98-0-0 98-0-0 98-0-0 98-0-0
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PRIOR APPLICATION NUMBER: 60/08959
PRIOR FILING DATE: 1998-66-17
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PRIOR PLING DATE: 1998-66-17
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PRIOR PLING DATE: 1998-66-18
PRIOR FILING DATE: 1998-66-18
PRIOR PLING DATE: 1998-66-18
PRIOR PLING DATE: 1998-66-18
PRIOR PLING DATE: 1998-66-19
PRIOR PLING DATE: 1998-66-22
PRIOR PLING DATE: 1998-66-23
PRIOR APPLICATION NUMBER: 60/09035
PRIOR APPLICATION NUMBER: 60/09035
PRIOR PLING DATE: 1998-66-24
PRIOR PLING DATE: 1998-66-25
PRIOR PLING DATE: 1998-60-26
PRIOR PLING DATE: 1998-60-60-36
PRIOR PLING DATE: 199

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APPLICATION NUMBER: 60/088028
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-03
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LICATION NUMBER: 60/088167
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FILING DATE: 1998-06-16
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APPLICATION NUMBER: 60/089600
FILING DATE: 1998-06-17
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LING DATE: 1998-06-10
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-17
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NG DATE: 1998-06-17
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APPLICATION NUMBER: 60/089801
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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3.6e-14;
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CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-13
PRIOR PLING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR PELING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065945
PRIOR FILING DATE: 1998-10-25
PRIOR PELING DATE: 1998-02-25
PRIOR PELING DATE: 1998-03-26
PRIOR PELING DATE: 1998-03-26
PRIOR PELING DATE: 1998-03-26
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083322
PRIOR APPLICATION NUMBER: 60/083322
                                                                                                                                                                                Query Match 90.7%; Score 166; DE Best Local Similarity 86.1%; Pred. No. 3.6e Matches 31; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                               RESULT 5
US-09-989-293A-403
Sequence 403 Application US/09989293A
PRETENT NO. US20020177164A1
GENERAL INFORMATION:
APPLICANT: AShkenazi, Avi J.
APPLICANT: Baker, Kevin P.
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/09178
PRIOR PILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-07
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APPLICATION NUMBER: 60/084600
APPLICATION NUMBER: 60/084600
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FILING DATE: 1998-05-28
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
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Eaton, Dan L.
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R FILING DATE: 1998-06-23

APPLICATION NUMBER: 60/090355

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R APPLICATION NUMBER: 60/090429

R FILING DATE: 1998-06-24

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R PALLICATION NUMBER: 60/090435
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FILING DATE: 1998-06-19
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
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APPLICATION NUMBER: 60/090678
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090690
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APPLICATION UNDBER: 60/090694
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
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FILING DATE: 1998-06-20
APPLICATION NUMBER: 60/090863
TITLE DATE: 1998-06-26
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APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091478
APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
                                                                                   FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948
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APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/090472
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APPLICATION NUMBER: 60/090535
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090540
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APPLICATION NUMBER: 60/090696
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APPLICATION NUMBER: 60/090862
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APPLICATION NUMBER: 60/091519
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APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
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APPLICATION NUMBER: 60/090254
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APPLICATION NUMBER: 60/090444
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APPLICATION NUMBER: 60/090542
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APPLICATION NUMBER: 60/091544
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APPLICATION NUMBER: 60/091626
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APPLICATION NUMBER: 60/091633
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APPLICATION NUMBER: 60/090252
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PLICATION NUMBER:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C61
                                                                                               Gaps
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                                                         Length 206;
                                                                                             Indels
                                                     Score 166; DB 9;
Pred. No. 3.6e-14;
4; Mismatches 1;
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CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997.10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997.11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997.11-13
                                                                                                                                                                                                                                                                   Sequence 403, Application US/09989735 Publication No. US20020193299A1 GENERAL INFORMATION:
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FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-37-09
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APPLICATION NUMBER: 60/084600
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APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
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Grimaldi, J.Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
                                                       Query Match 93.7%;
Best Local Similarity 85.1%;
Matches 31; Conservative
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Stewart, Timothy
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Gerritsen, Mary E
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APPLICATION NUMBER:
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FILING DATE APPLICATION APPLICATION FILING DATE APPLICATION	FILING DATE FILING DATE PRICATION FILING DATE PRILICATION FILING DATE APPLICATION FILING DATE FILING DATE PILING DATE APPLICATION FILING DATE	APPLICATION FILING DATE: PELING DATE: PELING DATE: PELING DATE: APPLICATION FILING DATE: APPLICA
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PRIOR APPLICATION NUMBER: 60/089948
PRIOR PELICATION NUMBER: 60/08952
PRIOR PELICATION NUMBER: 60/090246
PRIOR PELICATION NUMBER: 60/090246
PRIOR PELICATION NUMBER: 60/090252
PRIOR PELICATION NUMBER: 60/090254
PRIOR PELING DATE: 1998-06-22
PRIOR PELING DATE: 1998-06-23
PRIOR PELING DATE: 1998-06-23
PRIOR PELING DATE: 1998-06-23
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/09065
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090663
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090663
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE:

Query Match 90.7%; Score 166; DB 9; Length 206; Best Local Similarity 86.1%; Pred. No. 3.6e-14; Matches 31; Conservative 4; Mismatches 1; Indels 0;

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R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/08876

R FILING DATE: 1998-06-11

R PELLING DATE: 1998-06-12

R FILING DATE: 1998-06-12

R APPLICATION NUMBER: 60/089440

R FILING DATE: 1998-06-16

R FILING DATE: 1998-06-16

R FILING DATE: 1998-06-16

R FILING DATE: 1998-06-16

R FILING DATE: 1998-06-16
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R FILING DATE: 1998-06-09
R APPLICATION NUMBER: 60/088734
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088738
R FILING DATE: 1998-06-10
R PAPLICATION NUMBER: 60/088742
R FILING DATE: 1998-06-10
R PILING DATE: 1998-06-10
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089599
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APPLICATION NUMBER: 60/089653
FILING DATE: 1993-06-17
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FILING DATE: 1993-06-18
                           FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
APPLICATION OWHER: 1998-06-04
APPLICATION NUMBER: 60/088030
                                                                                                                    FILING DATE: 199E-06-04
APPLICATION NUMBER: 60/088033
FILING DATE: 199E-06-04
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APPLICATION NUMBER: 60/088212
FILING DATE: 199E-06-05
APPLICATION NUMBER: 60/088217
FILING DATE: 199E-06-05
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APPLICATION NUMBER: 60/089600
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APPLICATION NUMBER: 60/090246
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FILING DATE: 1996-06-04
APPLICATION NUMBER: 60/088167
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APPLICATION NUMBER: 60/088202
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APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/088858
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APPLICATION NUMBER: 60/088861
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APPLICATION NUMBER: 60/089907
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FILING DATE: 1993-06-19
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    APPLICATION NUMBER: 60/088028
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APPLICATION NUMBER: 60/088824
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  PRIOR HELDER HEL
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
RRVKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
                             CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11.14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065181
PRIOR APPLICATION NUMBER: 60/065111
PRIOR PILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
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R APPLICATION NUMBER: 60/084600
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/087106
R FILING DATE: 1998-05-28
R APPLICATION NUMBER: 60/087607
                                                                                                                                                                 Sequence 403, Application US/09990444 Publication No. US20020193300A1 APPLICANT: Ashkenazi,Avi J.
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APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/088025
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FILING DATE: 1998-02-25
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APPLICATION NUMBER: 60/087609
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PRIOR FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088021
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
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Desnoyers, Luc
Eaton, Dan L.
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Napier, Mary A.
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                                                                                                                                                                                                                                                                       Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Godowski, Paul
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US-09-990-444-403
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APPLICANT:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same File Reference: P2730P1C69 CURRENT APPLICATION NUMBER: US/09/989,730
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR PILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR PELLING DATE: 1997-11-12
PRIOR PELLING DATE: 1997-11-13
PRIOR PELLING DATE: 1997-11-13
PRIOR PELLING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065710
PRIOR APPLICATION NUMBER: 60/06570
PRIOR FILING DATE: 1997-11-24
PRIOR PELLING DATE: 1998-10-20
PRIOR PELLING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR PELLING DATE: 1998-04-28
PRIOR PELLING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087607
PRIOR APPLICATION NUMBER: 60/087607
PRIOR PELLING DATE: 1998-06-28
Application US/09989730
5. US20020197674A1
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FILING DATE: 1998-06-02
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy
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                          Publication No. US2C
GENERAL INFORMATION:
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Pred. No. 3.6e-14;
4; Mismatches 1;
                                PRIOR PETLICATION NUMBER: 60/090349
PRIOR PETLING DATE: 1998-06-23
PRIOR PELLING DATE: 1998-06-23
PRIOR PELLING DATE: 1998-06-23
PRIOR PELLING DATE: 1998-06-24
PRIOR PELLOATION NUMBER: 60/090445
PRIOR PELLING DATE: 1998-06-24
PRIOR PELLING DATE: 1998-06-24
PRIOR PELLING DATE: 1998-06-24
PRIOR PELLOATION NUMBER: 60/090540
PRIOR PELLING DATE: 1998-06-24
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PRIOR PELLING DATE: 1998-06-24
PRIOR PELLOATION NUMBER: 60/090540
PRIOR PELLING DATE: 1998-06-25
PRIOR PELLING DATE: 1998-06-26
PRIOR PELLING DATE: 1998-07-01
PRIOR PELLING DATE: 1998-07-02
PRIOR PELLING DATE: 1998-07-02
PRIOR PELLING DATE: 1998-07-03
PRIOR PELLING 
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R APPLICATION NUMBER: 60/090676

R PILING DATE: 1998-06-25

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Best Local Similarity 86.1<sup>3</sup>
Matches 31; Conservative
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APPLICATION NUMBER: 60/088029 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088030 FILING DATE: 1998-06-04 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088033 FILING DATE: 1998-06-04 FILING DATE: 1998-06-04 APPLICATION NUMBER:

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RESULT 8 US-09-989-730-403

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R APPLICATION NUMBER: 60/088202
R FILING DATE: 1998-06-05
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088212
R APPLICATION NUMBER: 60/088217
R APPLICATION NUMBER: 60/08855
R APPLICATION NUMBER: 60/08855
R FILING DATE: 1998-06-09
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R APPLICATION NUMBER: 60/088861
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/08876
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/089105
R APPLICATION NUMBER: 60/089105
R R PILING DATE: 1998-06-12
R APPLICATION NUMBER: 60/089440
R FILING DATE: 1998-06-16
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R APPLICATION NUMBER: 60/089538

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089598

R FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089952
FILLING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
FILLING DATE: 1998-06-22
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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090355
FILING DATE: 1998-06-23
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APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088858
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089801
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FILING DATE: 1998-06-18
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948
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FILING DATE: 1998-06-22
AAPPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
60/088326
                                   APPLICATION NUMBER: 60/088167
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-16
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                                                     1998-06-05
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                 FILING DATE: 1998-06-04
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Pred. No. 3.6e-14;
4; Mismatches 1;
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PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-24
PRIOR PAPLICATION NUMBER: 60/090431
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PRIOR APPLICATION NUMBER: 60/09045
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-25
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PRIOR PLING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/09069
PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09069
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PRIOR APPLICATION NUMBER: 60/09069
PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09069
PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09169
PRIOR PRILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/09169
PRIOR APPLICATION NUMBER: 60/09163
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86.18;
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Best Local Similarity 86.1
Matches 31; Conservative
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PRIOR FILING DATE: 1998-06-10
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PRIOR PELING DATE: 1998-06-17
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PRIOR PELING DATE: 1998-06-22
PRIOR PELING DATE: 1998-06-23
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APPLICATION NUMBER: 60/088742
FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088810
FILING DATE: 1998-06-10
                                                                                  PLICATION NUMBER: 60/088217
LING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088826
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/1
FILING DATE: 1998-06-24
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FULL REPERENCE: P3730F104
FUL
                                                                                                                                                                                         Godowski, Paul<sup>°</sup>J.
Grimaldi, J.Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                       Pan James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
Eaton, Dan L.
Ferrara, Napoleone
                                                                                               Gerber, Hanspeter
                                                                                                                             Gerritsen, Mary E
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                                                                                                                                                           Goddard, Audrey
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APPLICATION NUMBER: 60/090444

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APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPRENCE: P27301-53
CURRENT PAPLICATION NUMBER: US/09/991.181
CURRENT PELICATION NUMBER: US/09/991.181
PRIOR PLILIKE DATE: 2001-11-16
PRIOR PAPLICATION NUMBER: US/065186
PRIOR PLILIKE DATE: 1997-10-17
PRIOR PLILIKE DATE: 1997-10-17
PRIOR PLILIKE DATE: 1997-10-17
PRIOR PLILIKE DATE: 1997-10-17
PRIOR PAPLICATION NUMBER: (0/06331)
PRIOR PAPLICATION NUMBER: (0/078910
PRIOR PAPLICATION NUMBER: (0/08100
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APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
FILING DATE: 1998-06-05
FILING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088655
FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/088212
Grimaldi, J.Christopher
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Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                  Roy, Margaret Ann
Stewart, Timothy A
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                                                                                                         Napier, Mary A.
                                     Surney, Austin
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86.1%; Pred. No. 3.6e-14;
ive 4; Mismatches 1;
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                                                                                      R APPLICATION NUMBER: 60/090472

RR FILING DATE: 1998-06-24

RR APPLICATION NUMBER: 60/090535

RR APPLICATION NUMBER: 60/090540

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RR APPLICATION NUMBER: 60/090540

RR FILING DATE: 1998-06-24

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RR APPLICATION NUMBER: 60/090676

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RR FILING DATE: 1998-06-25

RR APPLICATION NUMBER: 60/090690

RR FILING DATE: 1998-06-25

RR APPLICATION NUMBER: 60/090690

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RR APPLICATION NUMBER: 60/090696

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RR FILING DATE: 1998-06-26

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091544
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
                          CATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/091626
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APPLICATION NUMBER: 60/091633
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APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/091982
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Gerber, Hanspeter
Gerritsen, Mary E.
                                                            FILING DATE: 1998-06-24
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Godowski, Paul J
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Eaton, Dan L.
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Best Local Similarity
Matches 31; Conserv
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PRIOR FILING DATE: 1998-06-10
PRIOR PRIOR PRICEATION NUMBER: 60/08862
PRIOR PRICEATION NUMBER: 60/08862
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PRIOR PAPLICATION NUMBER: 60/08861
PRIOR PAPLICATION NUMBER: 60/08861
PRIOR PAPLICATION NUMBER: 60/08962
PRIOR PLING DATE: 1998-06-11
PRIOR PAPLICATION NUMBER: 60/08967
PRIOR PLING DATE: 1998-06-16
PRIOR PLING DATE: 1998-06-17
PRIOR PAPLICATION NUMBER: 60/08959
PRIOR PLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08960
PRIOR APPLICATION NUMBER: 60/08998
PRIOR PLING DATE: 1998-06-17
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PRIOR APPLICATION NUMBER: 60/09035
PRIOR APPLICATION NUMBER: 60/09043
PRIOR PLING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/09044
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
FILING DATE: 1998-06-10
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; Length 206 1; Indels Query Match 90.7%; Score 166; DB 9; Best Local Similarity 86.1%; Pred. No. 3.6e-14; Matches 31; Conservative 4; Mismatches 1. 1 RRVKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36 PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR PAPLICATION NUMBER: 60/090676
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PAPLICATION NUMBER: 60/090690
PRIOR PILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-26
PRIOR FILING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-07
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
PRIOR PELING DATE: 1998-07-07 Sequence 403, Application US/09993687 Publication No. US20020198149A1 GENERAL INFORMATION: APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 Grimaldi, J. Christopher Botstein, David Desnoyers, Luc Eaton, Dan L. Ferrara, Napoleone Pan, James Paoni, Nicholas F. Roy, Margaret Ann Fong, Sherman Gerber, Hanspeter Gerritsen, Mary E Gurney, Austin L. Kljavin, Ivar J. APPLICANT: Ashkenazi, Avi J Baker, Kevin P. Goddard, Audrey Godowski, Paul Napier, Mary A. RESULT 11 US-09-993-687-403 qq á

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APPLICANT:

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R FILING DATE: 199E-06-10

R FILING DATE: 199E-06-10

R APPLICATION NUMBER: 60/08858

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R APPLICATION NUMBER: 60/08861

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R FILING DATE: 199E-06-11

R APPLICATION NUMBER: 60/08976

R FILING DATE: 199E-06-12

R APPLICATION NUMBER: 60/08940

R APPLICATION NUMBER: 60/08941

R APPLICATION NUMBER: 60/089512

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R FILING DATE: 1998-06-17

R APPLICATION NUMBIR: 60/089600

R FILING DATE: 1998-06-17

R APPLICATION NUMBIR: 60/089631

R FILING DATE: 1998-06-17

R APPLICATION NUMBIR: 60/089801

R FILING DATE: 1998-06-18

R APPLICATION NUMBIR: 60/089907

R FILING DATE: 1998-06-18

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R FILING DATE: 1998-06-18

R FILING DATE: 1998-06-19

R FILING DATE: 1998-06-19
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R APPLICATION NUMBER: 60/090246
R FILING DATE: 1998-06-22
R FILING DATE: 1998-06-22
R FILING DATE: 1998-06-22
R APPLICATION NUMBER: 60/090254
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R APPLICATION NUMBER: 60/090355
R FILING DATE: 1998-06-23
R APPLICATION NUMBER: 60/090429
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090431
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APPLICATION NUMBER: 60/090435
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
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APPLICATION NUMBER: 60/090349
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APPLICATION NUMBER: 60/090444
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APPLICATION NUMBER: 60/090445
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FILING DATE: 1998-06-24
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         PRILOGRAM
PRILOG
                                                                                                                                                                                 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C11
                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/993,687 CURRENT FILING DATE: 2002-11-14
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR PAPLICATION NUMBER: 60/065319
PRIOR PELING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PELING DATE: 1998-0.25
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PELING DATE: 1998-0.25
PRIOR APPLICATION NUMBER: 60/08450
PRIOR PELING DATE: 1998-0.25
PRIOR PELING DATE: 1998-0.25
PRIOR PELING DATE: 1998-0.25
PRIOR PELING DATE: 1998-0.07
PRIOR APPLICATION NUMBER: 60/088025
PRIOR PELING DATE: 1998-0.07
PRIOR APPLICATION NUMBER: 60/088025
PRIOR PELING DATE: 1998-0.07
PRIOR APPLICATION NUMBER: 60/088025
PRIOR PELING DATE: 1998-0.07
PRIOR APPLICATION NUMBER: 60/088026
PRIOR PELING DATE: 1998-0.07
PRIOR APPLICATION NUMBER: 60/088026
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PRIOR PELING DAT
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PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1000
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APPLICATION NUMBER: 60/088742
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FILING DATE: 1998-06-10
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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60/090540

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Acids Encoding the Same
                         FILE REFERENCE: P2730PIC64
CURRENT APPLICATION NUMBER: US/09/989,734
CURRENT FILING DATE: 2001-11-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR PAPLICATION NUMBER: 60/08332
PRIOR APPLICATION NUMBER: 60/084600
PRIOR APPLICATION NUMBER: 60/084600
PRIOR PELING DATE: 1998-05-07
PRIOR PAPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-05-07
PRIOR PELING DATE: 1998-06-02
PRIOR PELING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR APPLICATION NUMBER: 60/087609
PRIOR PELING DATE: 1998-06-02
PRIOR PELING DATE: 1998-06-02
PRIOR FILING DATE: 1998-06-03
PRIOR PELING DATE: 1998-06-03
PRIOR PELING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088021
PRIOR APPLICATION NUMBER: 60/088021
PRIOR PELING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR PELING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
                                                                                                                                                                                                                                                                                                            FILING DATE: 1997-11-12
APPLICATION UNMBER: 60/065311
FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/066770
                                                                                                                                       PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
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ING DATE: 1998-06-11
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091544
IR FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091519
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091626
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Publication No. US20030003531A1
GENERAL INFORMATION:
                                                                                                                            FILING DATE: 1998-06-25
APPLICATION UNMBER: 60/090694
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/090863
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
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FILING DATE: 1998-06-26
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APPLICATION NUMBER: 60/091633
FILING DATE: 1998-07-02
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FILING DATE: 1998-07-07
                                                                                               APPLICATION NUMBER: 60/090690
                                                                                                                                                                                                                                                                    FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090696
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Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Gerber, Hanspeter
Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1998-06-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 86.1
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baker, Kevin P.
Botstein, David
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PRIOR APPLICATION NUMBER: 60/08976
PRIOR PLING DATE: 1998-06-11
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PRIOR PLING DATE: 1998-06-16
PRIOR PLING DATE: 1998-06-17
PRIOR PLING DATE: 1998-06-19
PRIOR PLING DATE: 1998-06-22
PRIOR PLING DATE: 1998-06-22
PRIOR PLING DATE: 1998-06-23
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-25
PRIOR PLIN
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Sequence 2, Application US/10127966

Sequence 2, Application US/10127966

Bublication No. US20030003507A1

GENERAL INFORMATION:

APPLICANT: Baton, Dan L.

APPLICANT: Gurney, Austin L.

APPLICANT: Gurney, Austin L.

APPLICANT: Wood, William I.

PRICE OF INVENTION: Compositions and Methods for the Diagnosis and TITLE OF INVENTION: Treatment of Tumor.

FILE REFERENCE: P5034R1

CURRENT APPLICATION UNMBER: US/10/127,966

CURRENT FILING DATE: 1998-08-18

PRIOR FILING DATE: 1999-06-02

PRIOR FILING DATE: 2000-03-30

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-08-28

PRIOR FILING DATE: 2001-108-28

PRIOR FILING DATE: 2001-11-14

NUMBER OF SEQ ID NOS: 2

SED TD NO ? Gaps ; Length 206 Length 206; 1; Indels Score 166; DB 9; Pred. No. 3.6e-14; Score 166; DB 9; Pred. No. 3.6e-14; 4; Mismatches 1 44 RRVRDKDGDLKTQIEKLWTEVNALKEIQALQTVCLR 79 1 RRVKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36 PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR APPLICATION NUMBER: 60/090696
PRIOR PILING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR APPLICATION NUMBER: 60/091478
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR PELING DATE: 1998-07-07 90.7%; 36.1%; 90.78; 86.18; Query Match Best Local Similarity 36.11 Matches 31; Conservative ; ORGANISM: Homo Sapien US-10-127-966-2 Query Match Best Local Similarity q οy

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PRIOR APPLICATION NUMBER: 60/08029
PRIOR APPLICATION NUMBER: 60/08039
PRIOR PELING DATE: 1998-06-04
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PRIOR APPLICATION NUMBER: 60/089105
PRIOR PLILNG DATE: 1998-06-10
PRIOR PLILNG DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/089512
PRIOR PLILNG DATE: 1998-06-10
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   4; Mismatches
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Publication No. US20030008297A1
GENERAL INFORMATION:
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Gurney, Austin L.
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Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Roy, Margaret Ann
Stewart, Timothy A.
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Eaton, Dan L.
Ferrara, Napoleone
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Goddard, Audrey
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Gerber, Hanspeter
31; Conservative
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Botstein, David
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Matches
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Sequence 276, Application US/10174590 Publication No. US20030008352A1 GENERAL INFORMATION:

US-10-174-590-276

APPLICANT: Baker, Kevin P.

Chen, Jian

APPLICANT:

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Length 206;
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R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/090678
R APPLICATION NUMBER: 60/090690
R APPLICATION NUMBER: 60/090690
R FILING DATE: 1998-06-25
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FILING DATE: 1998-06-22
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-26
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FILING DATE: 1998-06-26
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FILLING DATE: 1938-07-01
APPLICATION NUMBER: 60/091478
FILLING DATE: 1998-07-02
60/090252
                                   FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/090355
FILING DATE: 1998-06-23
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/090429
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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FILING DATE: 1998-07-01
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-07
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FILING DATE: 1998-07-09
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Length 206; Indels

Score 166; DB 9; Pred. No. 3.6e-14; 4; Mismatches 1;

90.7%; 86.1%;

Query Match 90.7 Best Local Similarity 86.1 Matches 31; Conservative

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; ORGANISM: Homo Sapien US-10-174-590-276

SEQ ID NO 276

APPLICANT: Thang Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1-42
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2302-06-18
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612

Watanabe, Colin K. Wood, William I.

APPLICANT: APPLICANT:

Pan, James Smith, Victoria

APPLICANT: APPLICANT: APPLICANT:

Desnoyers, Luc Goddard, Audrey Godowski, Paul J. Gurney, Austin L.

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Search completed: April 15, 2003, 12:06:36
Job time : 11 secs
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Indels / Match 90.7%; Score 166; DB 9; Local Similarity 86.1%; Pred. No. 3.6e-14; nes 31; Conservative 4; Mismatches 1 1 RRVKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36 Best Loca Matches qq ò

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US-09-778-381-99
US-09-778-381-99
US-09-791-537-25686
US-10-177-293-55
PCT-US02-19669-57
US-09-981-18-10
US-09-981-2938-403
US-09-989-721-403
US-09-989-731-403
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APPLICANT: ELECTOUL, Thor Las
APPLICANT: Graversen, Niels Jonas Heilskov
APPLICANT: Kastrup, Jette Sandholm
APPLICANT: Larsen, Ingrid Kjoller
TITLE OF INVENTION: Trimerising module
FILE REFERENCE: THOGERSIEN =1
CURRENT APPLICATION: Trimerising module
FILE REFERENCE: 1000-07-17
CURRENT FILING DATE: 1098:06-11
PRIOR FILING DATE: 1999:06-11
PRIOR FILING DATE: 1999:06-11
PRIOR PILING DATE: 1908:06
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SOFTWARE: PALENTING VOS: 60
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2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

9: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

10: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

11: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

12: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

13: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

14: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*

15: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*

16: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*

17: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*

18: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*

19: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*

19: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*

10: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*

10: /cgn2_6/ptodata/1/paa/US09_COMB.pep:*

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/cgn2_6/ptodata/1/paa/US100_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US101_COMB.pep:*
/cgn2_6/ptodata/1/paa/US102_COMB.pep:*
/cgn2_6/ptodata/1/paa/US60_COMB.pep:*
                   GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                      - protein search, using sw model
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Gapop_10.0 , Gapext 0.5
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Match 1
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Length 36;

Score 183; DB 18; Pred. No. 7.2e-17;

100.0%; 100.0%;

Query Match Best Local Similarity

; ORGANISM: bovine US-09-445-576-37

Sequence 37, Appl Sequence 41, Appl Sequence 145359, Sequence 55, Appl Sequence 99, Appl Sequence 99, Appl

US-09-445-576-37 US-09-987-107-41 US-09-09-791-537-145359 PCT-USO2-19669-55 US-09-288-950-99 US-09-346-327-99

18 23 21 1 1 17

36 36 1197 1197 1197

100.0 100.0 100.0 90.7 90.7

183 183 166 166

Score

Result Š TYPE: PRT

Sequence 99, Appl Sequence 99, Appl Sequence 99, Appl Sequence 55, Appl Sequence 57, Appl Sequence 57, Appl Sequence 103, Appl

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APPLICANT: Millennium Pharmaceuticals, Inc. et al. TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o
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CURRENT APPLICATION NUMBER: US/09/288,950
CURRENT FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 101
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APPLICANT: Xu, Jiangchun
APPLICANT: Xi, Jiangchun
APPLICANT: Xi, Clangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
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Pred. No. 1.2e-13;
4; Mismatches 1;
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                                                                                        FILE REFERENCE: MAIL '0.08C', CURRENT APPLICATION NUMBER: PCT/US02/19669 CURRENT FILING DATE: 2002-06-21 PRIOR APPLICATION NUMBER: US 60/299, 887 PRIOR FILING DATE: 2001-06-21 PRIOR FILING DATE: 2001-06-27 PRIOR APPLICATION NUMBER: US 60/306,501 PRIOR FILING DATE: 2001-07-18 FILING APPLICATION NUMBER: US 60/305,002 PRIOR FILING DATE: 2001-07-18 FILING DATE: 2001-07-18 FILING DATE: 2001-07-18 FILING DATE: 2001-07-18 FILING APPLICATION NUMBER: US 60/362,585 PRIOR FILING DATE: 2002-05-05 PRIOR FILING DATE: 2002-05-14 NUMBER: US 60/3CXX,XXX PRIOR FILING DATE: 2002-05-14 NUMBER: US 60/3CXX,XXX PRIOR FILING DATE: 2002-05-14 NUMBER: US 60/XXX,XXX PRIOR FILING DATE: 2002-05-14 NUMBER: US 60/3CXX,XXX PRIOR FILING DATE: 2002-05-14 NUMBER: US 60/XXX,XXX PRIOR FILING DATE: 2002-05-14 NUMBER: US 60/XXX,XXX
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4; Mismatches
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GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
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86.1%;
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86.1%;
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Best Local Similarity 86.1
Matches 31; Conservative
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                                                                              FILE REFERENCE: MRI-038PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
PCT-US02-19669-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-288-950-99
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Best Local Similarity
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US-09-288-950-99
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTING DATE: 2001-03-22
SOFTWARE: PATENTING DATE: 2001-03-22
LENGTH: 197
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       Gaps
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     Indels
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Pred. No. 6e-16;
                                                                                                                                                                                                          Sequence 41, Application US/09987107
GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
APPLICANT: MOSETRUP, SOTEN
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR APPLICATION NUMBER: DK PA2001 00057
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
SOFTWARE: PatentIn version 3.1
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Pred. No. 7.2e
; Mismatches
     Mismatches
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Sequence 145359
Sequence 145359
SERERAL INFORMATION:
APPLICANT: Bionomix, Inc.
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PCT-US02-19669-55
Sequence 55, Application PC/TUS0219669
GENERAL INFORMATION:
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Best Local Similarity 100.0%; P

Matches 36; Conservative 0;
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Conservative
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US-09-791-537-145359
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Best Local Similarity
Matches 36; Conserv
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36;
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LENGTH: 36
Matches
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Gaps

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APPLICANT: Reed, Steven G.
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Dav.n C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: COMPOUNDS FOR BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.446D1
CURRENT APPLICATION NUMBER: US/09/745,288
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Xu, Jiangchin
APPLICANT: Xu, Jiangchin
APPLICANT: Davin C.
APPLICANT: Better, March W.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF BREAST CANCER
FILE REFERENCE: 210121.4467
CURRENT APPLICATION NUMBER: US/09/778,381
CURRENT APPLICATION NUMBER: 2001-02-06
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1.2e-13;
4; Mismatches 1; Indels (
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          Indels
          1;
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Pred. No. 1.2e-13;
4; Mismatches 1;
                                                                    35 RRVRDKDGDLKTQIEK:WTEVNALKEIOALOTVCLR 70
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        4; Mismatches
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                                                                                                                                                                     US-09-745-288-99; Sequence 99, Application US/09745288; GENERAL INFORMATION:
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86.1%;
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Best Local Similarity 86.1%;
Matches 31; Conservative
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Best Local Similarity 86.1
Matches 31; Conservative
        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
CORGANISM: Homo sapien
US-09-745-288-99
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        Matches
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: AL, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: AL, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
CURRENT APPLICATION NUMBER: US/09/687,507
CURRENT PILLIG DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 99
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GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Red, Steven G.
APPLICANT: Boillon, Davin C.
APPLICANT: Au, Jiangchun
APPLICANT: ALC COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF BREAST CANCER
FILE REPERENCE: 210.21.446C6
CURRENT APPLICATION NUMBER: US/09/687,507A
CURRENT FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 99
                                                                                                                                                                                                                                    Length 197;
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Pred. No. 1.2e-13;
4; Mismatches 1;
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Pred. No. 1.2e-13;
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Pred. No. 1.2e-13;
4; Mismatches 1;
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FILE REFERENCE: 210121.446C4
CURRENT APPLICATION NUMBER: US/09/346,327
CURRENT FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 99
LENGTH: 197
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86.1%;
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86.1%;
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Best Local Similarity 86.1%;
Matches 31; Conservative
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Best Local Similarity 86.15
Matches 31; Conservative
                                                                                                                                              TYPE: PRT
CORGANISM: Homo sapien
US-09-346-327-99
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; ORGANISM: Homo sapien
US-09-687-507-99
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US-09-687-507A-99
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Best Local Similarity
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US-09-687-507A-99
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Sequence 57, Application PC/TUS0219669
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc. et al.
APPLICANT: Millennium Pharmaceuticals, Inc. et al.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038PC
CURRENT APPLICATION NUMBER: PCT/US02/19669
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-27
PRIOR PRILICATION NUMBER: US 60/306,501
PRIOR PRILICATION NUMBER: US 60/306,501
PRIOR PRILICATION NUMBER: US 60/305,002
PRIOR PLILING DATE: 2001-09-16
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR PRILING DATE: 2002-03-05
PRIOR PRILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE FASTERQ for Windows Version 4.0
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APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Work Thomas D.
TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
FITLE OF INVENTION: Treatment of Tumor
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86.1%; Pred. No. 1.2e-13;
tive 4; Mismatches 1; Indels
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86.1%; Pred. No. 1.2e-13;
Live 4; Mismatches 1;
                                                                                   1 RRVKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
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CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 2
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Matches 31; Conservative
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APPLICANT: Eaton, Dan L.
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Best Local Similarity 86.1:
Matches 31; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo Sapien
PCT-US02-12619-2
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APPLICANT: Mantens, Maureen
APPLICANT: Myer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Wondyan
APPLICANT: Mondand: John
APPLICANT: Mondand: John
APPLICANT: Bast Jr., Robert C.
APPLICANT: Sahin, Ayaegul
APPLICANT: Sahin, Ayaeyul
A
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION WUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 25686
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SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 55, Application US/10177293
GENERAL INFORMATION:
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Kamatkar, Shubhangi
Mertens, Maureen
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                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-791-537-25686
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US-10-177-293-55
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Best Local Similarity
Matches 31; Conservat
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1998-06-11
IMBER: US 60/089,090
1998-06-12
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APPLICATION NUMBER: US bu/vos/c--
FILING DATE: 1998-06-16
---- MIMMFR: US 60/089,532
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APPLICATION NUMBER: US 60/089,653
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1998-06-24 .
WEBR: US 60/090,435
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MB3R: US 60/090,535
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IMBER: US 60/089,599
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IMBER: US 60/089,907
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MBI:R: US 60/089,948
1998-06-19
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MBER: US 60/090,246
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IMBER: US 60/090,252
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1998-06-11
"YBER: US 60/088,861
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1998-06-18
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IMPER: US 60/090,254
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MBER: US 60/090,431
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US 60/090,445
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US 60/090,538
     US 60/088,825
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FILING DATE: 1998-06-12
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   NN: Novel Polypeptides and Nucleic Acids Encoding the Same P2730R1C1
44 RRVRDKDGDLKTQIEKLWTEVNALKEIQALQTVCLR 79
                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/709,238
CURRENT FILING DATE: 2000-11-08
PRIOR PELING DATE: 1999-06-02
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PRIOR PELING DATE: 1998-06-02
PRIOR PELING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: US 60/087,827
PRIOR PELING DATE: 1998-06-03
PRIOR PELING DATE: 1998-06-04
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R PILING DATE: 1998-06-04
R APPLICATION NUMBER: US 60/088,030
R FILING DATE: 1998-06-04
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R APPLICATION NUMBER: US 60/088,033
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макк: US 60/088,810
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                                                                                        Sequence 403, Application US/09709238 GENERAL INFORMATION:
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FILING DATE: 1998-06-10
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Chen, Jian
Goddard, Audrey
Gurney, Austin
Smith, Victoria
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Wood, William I.
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FILING DATE: 1998-0
                                                                                                                                                                                                                                                               Yuan, Jean
                                                                                                                                                                                                                                                           APPLICANT: Yuan, Jes
TITLE OF INVENTION:
FILE REFERENCE: P27
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PRIOR PILING DATE: 1998-06-24

PRIOR PILICATION NUMBER: US 60/090,557

PRIOR PILICATION NUMBER: US 60/090,676

PRIOR PILICATION NUMBER: US 60/090,676

PRIOR FILING DATE: 1998-06-25

PRIOR FILING DATE: 1998-06-25

PRIOR PILICATION NUMBER: US 60/090,690

PRIOR FILING DATE: 1998-06-25

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PRIOR PELICATION NUMBER: US 60/090,692

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PRIOR PELICATION NUMBER: US 60/090,693

PRIOR PELICATION NUMBER: US 60/091,360

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PRIOR PELICATION NUMBER: US 60/091,360

PRIOR PELICATION NUMBER: US 60/091,626

PRIOR PELICATION NUMBER: US 60/091,636

PRIOR PELICATION NUMBER: US 60/091,637

PRIOR PELICATION NUMBER: US 60/091,939

PRIOR PELICATION NUMBER: US 60/091,939

PRIOR PELICATION NUMBER: US 60/093,339

PRIOR PELICATION NUMBER: US 60/093,339
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90.7%; Score 166; DB 21; Length 206;
Best Local Similarity 86.1%; Pred. No. 1.2e-13;
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps
1 RRVKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36

Db 44 RRVRDKDGDLKTGIBKLWTBVNALKEIQALGTVCLR 79

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Search completed: April 15, 2003, 12:04:10 Job time : 186 secs

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Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0% Database

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pending_Patents_AA_New:*

11. /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

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33. /cgn2_6/ptodata/2/paa/USO7_NEW_COMB.pep:*

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6. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

7. /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 276, Requence 276, Requence 276, Requence 276, Requence 276, Requence 39, Assequence 31, Assequence 27, Assequence 27 Sequence 403, Sequence 403, Sequence 276, Sequence 38, Sequence 57 Description Sequence Sequence (Sequence 3 Seguence Sequence Sequence Sequence Sequence US-09-445-576A-38
PCT-US02-19669A-55
PCT-US02-19669A-57
PCT-US02-19669A-57
US-09-989-733-403
US-10-125-923A-276
US-10-174-575-276
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US-10-194-486-276
US-10-194-486-276
US-09-445-576A-39
US-09-445-576A-37
US-09-445-576A-37 US-10-154-678-62 US-10-276-781-1559 US-09-445-576A-24 US-09-445-576A-35 PCT-US02-38407-13 US-09-992-095B-62 US-09-445-576A-25 JS-09-999-570-62 SUMMARIES ΩI DB Query Match Length [Score Result No.

PCT-US02-19669A-55

Sequence 55, Application PC/TUS0219669A
; Sequence 55, Application PC/TUS0219669A
; GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc. et al.
TITLE OF INVERTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT;
TITLE OF INVERTION: PREVENTION, AND THERAPY OF BREAST CANCER
TITLE OF INVERTION: FREVENTION, AND THERAPY OF BREAST CANCER
CURRENT APPLICATION NUMBER: PCT/US02/19669A
; CURRENT FILING DATE: 2001-06-21
; PRIOR FILING DATE: 2001-06-21
; PRIOR FILING DATE: 2001-06-27
; PRIOR PPLICATION NUMBER: US 60/301,572
; PRIOR APPLICATION NUMBER: US 60/305,002
; PRIOR APPLICATION NUMBER: US 60/305,002
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR PLING DATE: 2001-09-25
; PRIOR PLING DATE: 2001-09-25
; PRIOR PLING DATE: 2002-05-14
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506

Sequence

26 37, Appl 26 5, Appli 26 6, Appli 26 26, Appli 26 40, Appl 26 31, Appl 26 31, Appl 26 31, Appl 26 31, Appl 26 31, Appl 26 4184, A 26 421, Appl 26 421, Appl 26 9127, Appl 26 9127, Appli 27 9127, Appli 28 9127, Appli 29 9127, Appli 20 9127, Appli 20 9127, Appli 21 9127, Appli 22 9127, Appli 23 9127, Appli 26 9127, Appli 27 9127, Appli 28 9127, Appli 29 9127, Appli 20 9127, Appli 20 9127, Appli 21 9127, Appli 22 9127, Appli 23 9127, Appli 24 9127, Appli 25 9127, Appli 26 9127, Appli 27 9127, Appli 28 9127, Appli 29 9127, Appli 20 9127, Appli 20 9127, Appli 21 9127, Appli 22 9127, Appli 23 9127, Appli 24 9127, Appli 25 9127, Appli 26 9127, Appli 27 9127, Appli 28 9127, Appli 28 9127, Appli 29 9127, Appli 20 9127, Appli 20 9127, Appli 20 9127, Appli 21 9127, Appli 21 9127, Appli 22 9127, Appli 23 9127, Appli 24 9127, Appli 26 9127, Appli 27 9127, Appli 28 9127, Appli	; Gaps 0;	
sednence Sed	Length 36; Indels 0;	
27 76 41.5 36 5 US-09-445-576A-37 28 69 37.7 52 5 US-09-445-576A-5 30 64 35.0 75 52 5 US-09-445-576A-6 31 64 35.0 7 75 5 US-09-445-576A-6 32 60 32.8 105 09-445-576A-29 34 60 32.8 145 5 US-09-445-576A-29 34 60 32.8 145 5 US-09-445-576A-31 35 60 32.8 145 5 US-09-445-576A-31 36 60 32.8 145 5 US-09-445-576A-31 37 60 32.8 131 5 US-09-445-576A-31 38 11.7 459 5 US-09-445-576A-31 38 11.7 459 5 US-09-445-576A-31 39 58 31.7 459 5 US-09-445-576A-31 41 57.5 31.4 369 6 US-10-16-7293 41 57.5 31.1 209 7 US-60-452-680-1463B 43 57 31.1 209 7 US-60-453-135-9127 44 57 31.1 209 7 US-60-453-135-9127 45 57 31.1 209 7 US-60-453-135-9127 45 57 31.1 209 7 US-60-453-135-9127 46 57 31.1 474 6 US-10-094-749-3090 47 57 31.1 474 6 US-10-094-749-3090 48 57 31.1 EREPERENT ENTERORY Trimerising module FULLE OF INVENTION: Trimerising module FULLE OF INVENTION: Trimerising module FULLE OF INVENTION TRIMER: US-09-445,576A CURRENT FILING DATE: 2000-07-17 TYPE: PATEBER PATENTION US-09-07-17 TYPE: PATEBER PATENTION US-09-07-17 TYPE: PATENTION US-09-07-17 TYPE: PATENTION US-09-07-17 TYPE: PATENTION US-09-07-17 TYPE: PATENTION US-09-08-08-08-08-09-09-09-09-09-09-09-09-09-09-09-09-09-	%; Score 183; DB 5; %; Pred. No. 9.4e-20; 0; Mismatches 0;	RRVKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
6 41.5 36 5 US 9 37.7 73 52 5 US 4 35.0 49 5 US 4 35.0 65 5 US 2 32.9 36 5 US 2 32.9 36 5 US 0 32.8 33.0 5 US 0 33.1 209 7 US 7 31.1 209 7 US 7 31.1 209 7 US 7 31.1 474 6 US 0 USCATION: Trimerising ENCEAN UNMERRE US/0 LING DATE: 2000-07-17 SEQ ID NOS: 104 PatentIn version 3.1 6 BOVING BOVING A.38	100.0%; larity 100.0%; Conservative	KTQVEKLWREV
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APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
Acids Encoding the Same
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P730PLC8
FRICH APPLICATION NUMBER: 60/062260
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-24
PRIOR PLICATION NUMBER: 60/065311
PRIOR PLICATION NUMBER: 60/065310
PRIOR APPLICATION NUMBER: 60/065310
PRIOR APPLICATION NUMBER: 60/06910
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075910
PRIOR PLING DATE: 1998-03-20
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pred. No. 2.5e-16;
4; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 403, Application US/09992643
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ferrar, Napoleone
Forng, Sherman
Gerber, Hanspeter
Geritsen, Mary E.
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Pan, James
Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.7%;
Best Local Similarity 86.1%;
Matches 31; Conservative 4
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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                                                               Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Desnoyers, Luc
                                                                                                                                     Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-09-989-733-403
Napier, Mary A.
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APPLICANT:
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APPLICANT:
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Sequence 57, Application PC/TUS0219669A
Sequence 57, Application PC/TUS0219669A
Sequence 57, Application Plarmaceuticals, Inc. et al.
GENERAL INFORMATION:
APPLICATION:
APPLICATION:
TITLE OF INVENTION:
FILE REFERENCE: MRI-038PC
CURRENT PILING DATE: 2001-06-21
CURRENT PLING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR PLILING DATE: 2001-06-21
PRIOR PPLICATION NUMBER: US 60/306,501
PRIOR PPLICATION NUMBER: US 60/306,501
PRIOR APPLICATION NUMBER: US 60/305,501
PRIOR PLILNG DATE: 2001-06-21
PRIOR PPLING DATE: 2001-06-21
PRIOR PPLICATION NUMBER: US 60/305,501
PRIOR PPLICATION NUMBER: US 60/305,502
PRIOR PPLICATION NUMBER: US 60/305,503
PRIOR PLILNG DATE: 2001-09-25
PRIOR PLILNG DATE: 2001-09-25
PRIOR PLILNG DATE: 2002-03-05
PRIOR PLILNG DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR PRIOR DATE: 2002-03-05
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                                                                                                                                                                                                                           Length 197;
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                                                                                                                                                                                                                                                                                                                                         Godowski, Paul<sup>*</sup>J.
Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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GENERAL INFORMATION:
                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 55
LENGTH: 197
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pcr-us02-19669A-57
                                                                                                                                                                                            ORGANISM: Homo sapiens
pcr-US02-19669A-55
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US-09-989-733-403
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       APPLICANT: Tumes, Daniel
APPLICANT: Tumes, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Watliams, P. Mickey
APPLICANT: Walliams, P. Mickey
APPLICANT: Walliams, P. Mickey
APPLICANT: Walliams, P. Mickey
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC13
CURRENT APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
PRIOR PELICATION NUMBER: 60/081106
PRIOR FILING DATE: 1998-05-07
PRIOR PELICATION NUMBER: 60/081106
PRIOR FILING DATE: 1998-05-07
PRIOR PELICATION NUMBER: 60/081106
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-08
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1079
CURRENT APPLICATION NUMBER: U5/10/125,923A
CURRENT FILING DATE: 2002-01-15
PRIOR PPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 10/052586
PRIOR FILING DATE: 10/05263
PRIOR FILING DATE: 1997-09-18
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Pred. No. 2.5e-16;
4; Mismatches 1
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Timothy A.
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86.1%;
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Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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Best Local Similarity 86.1%
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Smith, Victoria
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ORGANISM: Homo sapiens
US-09-992-643-403
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Sequence 276, Applica
GENERAL INFORMATION:
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APPLICANT:
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APPLICANT: ABOUNTILIANI 1.

APPLICANT: ABOUNTILIANI 1.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODIN; THE SAME FILLE OF INVENTION: ACIDS ENCODIN; THE SAME FILLE OF INVENTION: ACIDS ENCODIN; THE SAME FILLE PREPRENCE: P9430R4C517

CURRENT PILLING DATE: 2002-07-26

PRIOR PAPLICATION NUMBER: 00/05236

PRIOR FILLING DATE: 1997-00-18

PRIOR PILLING DATE: 1997-00-18

PRIOR PILLING DATE: 1997-00-18

PRIOR FILLING DATE: 1997-00-18

PRIOR PILLING DATE: 1997-00-17

PRIOR PILLING DATE: 1997-10-17

PRIOR PILLING DATE: 1997-10-24

PRIOR PILLING DATE: 1997-10-28

PRIOR PILLING DATE: 1997-10-28
PRIOR FILING DATE: 1997-09-18

PRIOR PLICATION NUMBER: 60/06250

PRIOR PAPLICATION NUMBER: 60/063120

PRIOR FILING DATE: 1997-10-14

PRIOR PLING DATE: 1997-10-24

PRIOR PLING DATE: 1997-10-24

PRIOR PLING DATE: 1997-10-24

PRIOR PLING DATE: 1997-10-24

PRIOR PLING DATE: 1997-10-28

PRIOR PRIOR APPLICATION NUMBER: 60/063541

PRIOR PLING DATE: 1997-10-28

PRIOR PLING DATE: 1997-10-28
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Pred. No. 2.5e-16;
4; Mismatches 1.
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86.1%;
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Watanabe, Colin K.
Wood, William I.
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Godowski, Paul J
Gurney, Austin L
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; ORGANISM: Homo Sapien
US-10-125-923A-276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Ouery Match Best Local Similarity 90.7%; Score 166; DB 6; Length 20¢ Matches 31; Conservative 4; Mismatches 1; Indels 1 RRVKEKDGDLKTQVEKLMREVNALKEMQALGTVCLR 36 44 RRVRDKBCBLKTQIEKLWTEVNALKEIGALOTVCLR 79 Sequence 276, Application US/10187755 Baker, Kevin p. Chen, Jian

Ouery Match
Beet Local Similarity 90.7%; Score 166; DB 6; Length.206;
Aatches 31; Conservative 4; Mismatches 1; Indels

TYPE PRT ORGANISM: HOMO Sapien

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Matches
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CURRENT APPLICATION NUMBER: US/10/187,749
CURRENT APPLICATION NUMBER: US/10/052,586
PRIOR APPLICATION NUMBER: US/10/052,586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1097-09-18
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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SEQ ID NO 276
LENGTH: 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 2.5e-16;
4; Mismatches J
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                                       TILLE REFERENCE: 9430R11

CURRENT APPLICATION NUMBER: US/10/187,755

CURRENT APPLICATION NUMBER: US/10/187,755

CURRENT APPLICATION NUMBER: US/10/187,755

CURRENT APPLICATION NUMBER: US/10/052,586

PRIOR FILING DATE: 1907-09-18

PRIOR PLING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/05926

PRIOR PLING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/06326

PRIOR FILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-10-24

PRIOR PLING DATE: 1997-10-28

PRIOR PLING DATE: 1997-10-28

PRIOR PLING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063540

PRIOR PLING DATE: 1997-10-28

PRIOR PLING DATE: 1997-10-28
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PRIOR APPLICATION UNBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
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APPLICATION NUMBER: 60/063120
FILING DATE: 1997-10-24
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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86.1%;
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Gurney, Austin L.
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Best Local Similarity 86.15
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-187-755-276
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Built, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Lang, Zemin
TITLE OF INVENTION: BECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: BECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/199, 672
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/05926
PRIOR FILING DATE: 1997-09-18
PRIOR PRILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/063250
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR PRILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR PRILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR PRILING DATE: 1997-10-28
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PRIOR FILING DATE: 1997-10-24
PRIOR PELLING DATE: 1997-10-24
PRIOR PELLICATION NUMBER: 60/063486
PRIOR PELLICATION LONDER: 60/063540
PRIOR APPLICATION NUMBER: 60/063541
PRIOR PELLING DATE: 1997-10-28
PRIOR PELLING DATE: 1997-10-28
PRIOR PELLING DATE: 1997-10-28
PRIOR PELLING DATE: 1997-10-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 276
LENGTH: 206
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SEQ ID NO 276

LENGTH: 206

TYPE: PRT

ORGANISM: Homo Sapien
US-10-199-672-276
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Pred. No. 2.5e-16;
4; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RRVKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
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86.18;
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                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo Sapien
US-10-187-749-276
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Best Local Similarity
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TYPE: PRT
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C1
                                                Gaps
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SEQ ID NO 276
                                              ;
      Length 206;
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                                            1; Indels
  Score 166; DB 6;
Pred. No. 2.5e-16;
4; Mismatches 1.
                                                                       1 RRVKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/194,486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: US/10/052,586
PRIOR FILING DATE: 2002-01-15
                                                                                                                                                                                                                    Sequence 276, Application US/10194486
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/062250
FILING DATE: 1997-10-17
PPLICATION NUMBER: 60/063120
FILING DATE: 1997-10-24
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FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/063486
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PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
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PRIOR FILING DATE: 1997-10-28
FREMBAING DATE: 1997-10-20
Query Match 90.7%;
Best Local Similarity 86.1%;
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Watanabe, Colin K.
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Godowski, Paul J.
Gurney, Austin L.
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Smith, Victoria
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; ORGANISM: Homo Sapien
US-10-194-486-276
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Matches 31; Conserv
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US-10-194-486-276
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APPLICANT: Borean Pharma A/S TITLE OF INVENTION: Trimerising module

Sequence 39, Application US/09445576A GENERAL INFORMATION:

US-09-445-576A-39

RESULT 14

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Gaps
                                                                                                                                                                                                                       Length 36;
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3.1e-11;
2;
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; FILE REFERENCE: 62032.000004

; CURRENT APPLICATION NUMBER: US/09/445,576A

; CURRENT FILING DATE: 2000-07-17

; NUMBER OF SEQ ID NOS: 104

; SOFTWARE: Patentin version 3.1

; ENGTH: 36

; TYPE: PRT

; CRGANISM: Shark

US-09-445-576A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Borean Pharma A/S

TITLE OF INVENTION: Trimerising module
FILE REFERENCE: 62032,000004

CURRENT APPLICATION NUMBER: US/09/445,576A

CURRENT FILING DATE: 2000-07-17

NUMBER OF SEQ ID NOS: 104

SOFTWARE: Patentin version 3.1

SEQ ID NO 36

LENGTH: 36
                                                                                                                                                                                                                     Score 124.5;
Pred. No. 3.16
6; Mismatches
                                                                                                                                                                                                                                                                                                                 4 KEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: April 15, 2003, 12:05:48
Job time: 24.25 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36, Application US/09445576A GENERAL INFORMATION:
                                                                                                                                                                                                                   68.08;
72.78;
                                                                                                                                                                                                                                                       24; Conservative
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Best Local Similarity 57.1
Matches 16; Conservative
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                                                                                                                                                                                                             Query Match
Best Local Similarity
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us-09-445-576a-38.rpr

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April 15, 2003, 11:45:44 ; Search time 11.75 Seconds (without alignments) 294.540 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                     283224
GenCore version 5.1.4-p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                               US-09-445-576A-38
183
1 RRVKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                       283224 seqs, 96134422 residues
                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0 Maximum DB seq length: 20000000000
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                                                                                                                                                                                                                                                                 Sequence:
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                                                                                                                               Run on:
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Maximum Match 100% Listing first 45 summaries 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR_73:* Database :

Post-processing: Minimum Match 0%

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

	Description	tetranectin homolo			probable transcrip	conserved hypothet	ABC transporter AT	hypothetical prote	heat shock transcr	heat shock transcr	lipoprotein [impor	related to Nup98-N	cell-cycle-depende	conserved hypothet	structural mainten	hypothetical prote	conserved hypothet	hypothetical prote	_	Ħ	hypothetical prote	hypothetical prote		_	,	hypothetical coile	hypothetical prote	insulin II gene en	acetyl-CoA carboxy	keratin 8, type II
SUMMARIES	ID	A37289	TTHUN	JC4031	T38023	H72310	G97579	AE2800	B40583	A41138	D90551	T51890	PC4035	D69104	T47626	D83769	G69002	AB0443	T34142	F64662	S57536	T01546	T01798	G84587	T17430	T50451	G84868	T48845	E84045	S05474
	DB	1	1	~	N	ď	~	~	7	7	~	~	7	~1	~	7	Н	7	~	ď	~	~	~	~	~	~	7	7	~	7
	Length	166	202	202	630	1008	251	251	517	536	631	1844	1017	73	1265	156	306	391	629	759	102	319	862	916	1011	952	520	686	325	489
đ	Ouery Match	68.0	43.2	41.5	35.5	33.3	32.2	32.2	31.7	31.7	31.7		30.9		30.3	30.1	30.1	30.1			29.2				29.5	29.5	29.0	28.7	28.4	28.4
	Score	124.5	79	16	65	61	59	59	58	58	58	57.5	56.5	26	55.5	52	52	52	54.5	•	54	24	24	54	54	53.5	S	52.5	52	25
	Result No.	1	7	3	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT 2

tetranectin precursor [validated] - human
N;Alternate names: plasminogen-kringle 4 binding protein
C;Species: Homo Saplans (man)
C;Date: 30-Jun-1992 #sequence_revision 03-Aug-1995 #text_change 08-Dec-2000
C;Accession: S24126; A56835; A29747; I38359; S19865
R;Berglund, L.; Petersen, T.E.
FBS Lett. 309, 15-19, 1992
A;Title: The gene structure of tetranectin, a plasminogen binding protein.
A;Reference number: S24126; MUID:92380263; PMID:1511740
A;Accession: S24126
A;Molecule type: DNA
A;Residues: 1-202 <BREN
A;Cross-references: EMBL: X70911
R;Wewer, U. M.; Albrechtsen, R.
Lab. Invest. 67, 253-262, 1992
A;Title: Tetranectin, a plasminogen kringle 4-binding protein. Cloning and gene exprances: number: A56835; MUID:92365345; PMID:1354271
A;Accession: A56835; MUID:92365345; PMID:1354271

A;Molecule type: mRNA A;Residues: 1-202 <WEM> A;Cross-references: EMBL:X64559; NID:g37408; PIDN:CAA45860.1; PID:g37409 A;Experimental source: placenta R;Fuhlendorff, J.; Clemmensen, I.; Magnusson, S.

hypothetical prote plexin 3 precursor intermediate filam endopeptidase Clp hypothetical prote karyopherin beta myosin heavy chain transliin - chicke plexin 2 precursor superoxide dismuta	RESULT 1 A13789 A23789 tetranectin homolog - reef shark C;Species: Carcharhinus springeri (reef shark) C;Species: Carcharhinus springeri (reef shark) C;Date: 10.580-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A37289; A37289 C;Accession: A37289; A37289 A;Title: Primary structure of a protein isolated from reef shark Carcharhinus springeringering structure of a protein losolated from reef shark Carcharhinus springeringering A;Reference number: A37289; MUID:93284081; PMID:1304877 A;Accession: A37289 A;Accesion: A37289 A;Accession: A37289 A;Accession:
D71853 JC4976 S51157 S76431 A82086 E84035 E84035 T34177 T34177 T34177 MHCH MHCH S74886 F81191 159350 A2224 A22091 JC4975 S48831	n homolog - reef shark Carcharhinus springeri (reef shark) -sep-1999 #sequence_revision 10-sep-1 i. 1, 161-168, 1992 i. 1, 161-168, 1992 n. A37289; MJD:93284081; PMID n. A37289; MUD:93284081; PMID n. A37289
оприновироворо	ark geri reeg a g ulb ulb ulb ulb ulb ulb ulb ulb ulb ulb
1884 - 1884	og - reef shark rhinus springeri 99 #sequence_ree 89; A37287 ung, C.N.; Treef 61-168, 1992 structure of a Fr: A37289; MUID 89 R99 R99 R99 R90 R02> ris A37289; MUID R02> rectin cNE2> remectin; C-tyl 1age C-type lectin hc 6-152/Disulfide 6-152/Disulfide 6-152/Disulfide 1arity 72.7%; Conservative 1:::
28	innumin #s
98886777777777777	1999 1999
52 51.5 51.5 51.5 51.5 51.5 51.5 51.5 51	RESULT 1 AA37289 tetranectin homolog - reef shark C; Species: Carcharhinus springeri (reef C; Accession: A37289; A37287 R; Neame, P.J.; Young, C.N.; Treep, J.T. R; Neame, P.J.; Young, C.N.; Treep, J.T. R; Neame, P.J.; Young, C.N.; Treep, J.T. A; Title: Primary structure of a protein A; Reference number: A37289; MUD:9328408 A; Accession: A37289 A; Molecule type: protein A; Residues: 1-166 <ne2> C; Superfamily: tetranectin; C-type lecti C; Superfamily: Tetranectin; C-type lectin; Superfamily: Superfamily: Tetranectin; C-type lectin; Superfamily: Sup</ne2>
; 0110 0110 0110 0110 0110 0110 0110 01	RESULT 1 A37289 tetranect C;Species C;Date: 1 C;Accessi R;Neame, Protein S AT118: A;Referen A;Re
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Gaps

10;

Indels

Length 630;

Score 65; DB 2; Pred. No. 2.4; 6; Mismatches

us-09-445-576a-38.rpr

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conserved hypothetical protein - Thermotoga maritima (strain MSBB)
C;Species: Thermotoga maritima
C;Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: H72310
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-1008 <arn>
A;Cross-references: GB:AE001760; GB:AE000512; NID:g4981510; PIDN:AAD36066.1; PID:g498
A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUD:99287316; PMID:10360571 A;Accession: H72310 A;Status: preliminary
                A;Residues: 1-630 <MUR>
A;Cross-references: EMBL:298598; PIDN:CAB11234.1; GSPDB:GN00066; SPDB:SPAC1B3.05
A;Experimental source: strain 972h-; cosmid c1B3
                                                                                                                                                                                                                                                                                                                                                                                                                      -- WREVNALKEMOAL 30
                                                                                                                                                                                                                                                                   35.5%;
ilarity 43.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                          4 KEK-DGDLKTQVEKL-----
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Best Local Similarity 43.88
Matches 14; Conservative
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Best Local Similarity 41.54
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 399, 323-329, 1999
                                                                                                         C;Genetics:
A;Gene: SPDB:SPAC1B3.05
A;Map position: 1
A;Introns: 75/3
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
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Biochemistry 26, 6757-6764, 1987
A'Ille: Primary structure of tetranectin, a plasminogen kringle 4 binding plasma protei
A'Reference number: A29747; MUID:88107595; PMID:3427041
A'Accession: A29747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cipacies: Mus musculus (house mouse)
Cipacies: Mus musculus (house mouse)
Cipacies: Mus musculus (house mouse)
Cipacies: Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Aug-1999
CiAccession: Jun-1995
Riscensen, C.B.; Berglund, L.; Petersen, T.E.
Gene 152, 243-245, 1995
A;Title: Cloning of a cDNA encoding murine tetranectin
A;Reference number: JC4031; MUD:95137396; PMID:7835708
A;Reference number: JC4031
A;Molecule type: mRNA
A;Residues: 1-202 <SOR>
A;Residues: 1-202 <SOR>
A;Residues: 1-202 <SOR>
A;Reperimental source: lung
C;Comment: This protein binds plasminogen, and may play a role in invasive cancer.
C;Superfamily: tetranectin; C-type lectin homology
F;1-21/Domain: signal sequence #status predicted <SIG>F;22-202/Product: tetranectin #status predicted <AMT>
F;1-197/Domain: C-type lectin homology <LCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: tetramectin; C-type lectin homology
C; Keywords: glycoprotein; plasma; tetramer
C; Keywords: glycoprotein; plasma; tetramer
F; 1-21/Domain: signal sequence #status predicted <SIG>
F; 2-202/Product: tetramectin #status experimental <MAT>
F; 1-197/Domain: C-type lectin homology <LCH>
F; 25/Binding site: carbohydrate (Thr) (covalent) #status experimental
F; 71-81,98-197,173-189/Disulfide bonds: #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.5%; Score 76; DB 2; Length 202; 57.1%; Pred. No. 0.031;
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A;Molecule type: DNA
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                                                                                                                   A Residues: 22-105, 'G', 107-202 <FUH>
C Genetics: 5- Ser and 58-Met were also found C; Genetics: A Gene: GDB:TNA
A; Gross-references: GDB:135032; OMIM:187520
A; Map posttion: 3922-3921.3
A; Introns: 37/1; 70/1
C; Complex: homotetramer
C; Superfamily: tetranectin; C-type lectin homol C; Keywords: 91ycoprotein; plasma; tetramer
F; 1-21/Domain: signal sequence #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 DLKTQVEKLWREVNALKEMQALQTVCLR 36
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Matches 1
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ABC transporter ATP-binding protein XF1475 [imported] - Agrobacterium tumefaciens (st C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C; Accession: G95759
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: circular chromosome
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A;Reference number: A97359; PMID:11743194
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A,Molecule type: DNA
A,Residues: 1-251 <KUR>
A,Cross-references: GB:AE007869; PIDN:AAK87592.1; PID:915156934; GSPDB:GN00169
                                                                                                                                         Gaps
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                                                                                    Length 1008;
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A;Gene: TM0987
C;Superfamily: conserved hypothetical protein PH0905
                                                                                 DB
13;
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3; Mismatches
                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                     :|| ||||||| ::|| 344 KVKVKDGDLIFEPATKEDSEKLWKAKEKVREM 375
                                                                                                                                                                                      2 RVKEKDGDL-----KTQVEKLWREVNALKEM 27
                                                                                 Score 61;
Pred. No.
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41.5%; Pred. No.
                                                                              33.3%;
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Wed Apr 16

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R;Schuetz, T.J.; Gallo, G.J.; Sheldon, L.; Tempst, P.; Kingston, R.E. Proc. Natl. Acad. Sci. U.S.A. 88, 6911-6915, 1991
A;Title: Isolation of a cDNA for HSF2: evidence for two heat shock factor genes in hu A;Reference number: A41138; MUID:91334377; PMID:1871106
A;Accession: A41138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cydrosesion: D90531
Rychambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, Nucleic Acids Res. 29, 2145-2153, 2001
Rychambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, Nucleic Acids Res. 29, 2145-2153, 2001
A.; Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma p A; Reference number: A99512; MUID:21267165; PMID:11353084
A; Recession: D90551
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-631 < KUR>
A; Residues: 1-631 < KUR>
A; Cross-references: GB:AL445566; PID:g14089730; PIDN:CAC13489.1; GSPDB:GN00153
A; Experimental source: strain UAB CTIP
A; Genetics: A; Gene: MYPU.3160
A; Genetic code: SGC3
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Nalternate names: protein B23111.20
C.Species: Neurospora crassa
C.Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C.Accession: T51890
C.Accession: T51890
C.Accession: T51890
C.Accession: T51890
A.Reference number: 225858
A.Ref
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C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
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                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-536 <SCH>
A; Residues: 1-536 <SCH>
A; Cross-references: GB:M65217; NID:g184404; PIDN:AAA36017.1; PID:g184405
C; Genetics: A; Gene: GB:HSF2
A; Cross-references: GDB:128716; OMIM:140581
A; Cross-references: GDB:128716; OMIM:140581
C; Superfamily: HSF DNA-binding domain homology
C; Keywords: DNA binding; transcription regulation
F;10-116/Domain: HSF DNA-binding domain homology <HSF>
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Pred. No. 19;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :: ::||::|||:||:||:||
143 IESRLSELKSENESLWKEVSELRAKHAQQQQVIR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 VKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56
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52.4%;
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Best Local Similarity
Matches 11; Conserva
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Best Local Similarity
Matches 11; Conserv
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A;Map position: 6
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T51890
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A.Accession: 840583
A.Accession: 840583
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-517 <SAR>
A.Residues: 1-517 <SAR>
C.Cross-references: GB:X61754; NID:951447; PIDN:CAA43893.1; PID:951448
C.Superfamily: HSF DNA-binding domain homology
C.Keywords: DNA binding; transcription regulation
F;10-116/Domain: HSF DNA-binding domain homology <HSF>
                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, F.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: circular chromosome
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
                                                                                                                                                                                                                                                                                      hypothetical protein sufC [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ster, E.W.
A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Reference number: AB2577; PMID:11743193
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-251 < KUR>
A; Cross-references: GB: AE008688; PIDN: AAA42819.1; PID: 917740265; GSPDB: GN00186
A; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                  C.Species: Agrobacterium tumefaciens
C.Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heat shock transcription factor HSF2 - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_qhange 05-Nov-1999
C;Accession: A41138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.2%; Score 59; DB 2; Length 251; Best Local Similarity 41.5%; Pred. No. 5.3; Matches 17; Conservative 3; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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R; Sarge, K.D.; Zimarino, V.; Holm, K.; Wu, C.; Morimoto, R.I.
Genes Dev. 5, 1902-1911, 1991
                                                        1 RRVKEKDGDLKTQVEKLWREVNA-----LKEMQALQTVCL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RRVKEKDGDLKTQVEKLWREVNA-----LKEMQALQTVCL 35
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Matches 11; Conserv
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Nyllernate names: protein TSN23.30
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T47626
R;Obermaier, B; Ottenwaelder, B; Duchemin, D; Zeitler, K; Mewes, H.W.; Lemcke, K. submitted to the Protein Sequence Database, March 2000
A;Reference number: 224463
A;Accession: T47626
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1265 <OBE>
A;Residues: 1-1265 <OBE>
A;Cross.references: EMBL:AL138650
A;Experimental source: cultivar Columbia; BAC clone T5N23
C;Genetics:
A;Map position: 3
A;Introns: 14773; 226/3; 312/3; 392/2; 481/2; 571/3; 620/3; 670/1; 766/1; 752/3; 784/A;Note: T5N23.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R'Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-156 <STO>
A;Cross-references: GB:AP001510; GB:BA000004; NID:gl0173440; PIDN:BAB04675.1; GSPDB:G
A;Experimental source: strain C-125
                                             structural maintenance of chromosomes (SMC)-like protein - Arabidopsis thallana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Bacillus halodurans
C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein BH0956 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.1%; Score 55; DB 2; 50.0%; Pred. No. 10;
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Pred. No. 79;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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Best Local Similarity 37.59
Matches 12, Conservative
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Best Local Similarity
Matches 10; Conserv
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Blochem. Blophys. Res. Commun. 212, 220-228, 1995
A:Title: A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal domain suffici
A:Accession: Pc4035; MUID:95336446; PMID:7612011
A:Accession: Pc4035
A:Molecule type: DNA
A:Residues: 1-1017 <LIO>
A:Residues: 1-1017 <LIO>
A:Residues: 1-1017 <LIO>
A:Cross-references: GB:U25725; NID:9818866; PIDN:AAA86889.1; PID:9818867
A:Note: repeat 15-160 and 200-340
C:Comment: This protein contains a coiled-coil and a globular domain at the carboxy-term C:Keywords: nucleoprotein; phosphoprotein
F:465/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase) #statu F:985,836,838/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status pu
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R. Smith, D. R.; Doucette-Stamm, L. A.; Deloughery, C.; Lee, H.; Dubois, J.; "Aldredge, T.; Qlu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. J. Bacteriol. 179, 7135-7155, 1997
A. Bacteriol. 179, 7135-7155, 1997
A. Fieler Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A. Accession: D63104
A. Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Cross-references: GB:AE000933; GB:AE000666; NID:g2622908; PIDN:AAB86244.1; PID:g262290
A;Experimental source: strain Delta H
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                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 08-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
                                                                                                                          Gaps
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                                                                 Length 1844;
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                                                                 DB 2;
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ilarity 43.8%; Pred. No. 47;
Conservative 7; Mismatches
                                                                                                                  2; Mismatches
                                                              Score 57.5;
Pred. No. 66;
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Pred. No. 3
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                                                                                                                                                                                                  Query Match 31.4%;
Best Local Similarity 63.2%;
Matches 12; Conservative ;
                                                                                                                                                                  DLKTQVEKLWREVNALKEM 27
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Best Local Similarity 44.4%;
Matches 12; Conservative
A; Introns: 34/1; 1281/3
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nes 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: PC4035
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A;Gene: MTH1778
A;Start codon: GTG
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Best Local S
Matches 14
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Indels

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Length 1265;

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us-09-445-576a-38.rsp

Page 1

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April 15, 2003, 11:44:09 ; Search time 6.5 Seconds (without alignments) 229.715 Million cell updates/sec
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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183
1 RRVKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                            OM protein - protein search, using sw model
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Perfect score:
Sequence:
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112892 seqs, 41476328 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	a ID					1 HSF2_MOUSE			SMB2																		HSE		HSF	PEPO_	PEPO	RRPO_	- 1	MAFK_CHICK
	Length DB	197																				206											81	
æ	Query					31.7		•				•	•	٠		٠		•				27.3												27.0
	Score	16	124.5	79	97	28	28	54	52.5	52	51	51	51	51	51	21	51	50.5	50.5	50.5	50.5	20	20	20	20	20	20	20	20	20	20	S	49.5	6
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884 1 SMX5_SCHMA 561 1 NCAP_PIARV 570 1 NCAP_LASSG 993 1 SMB2_MOUSE 123 1 YB44_YEAST 770 1 VIM1_CARAU 233 1 RZ_GALSU 533 1 NUME_PIG 802 1 CC21_XENLA 802 1 CC22_XENLA 802 1 CDC2_RANDY 448 1 VIME_CRIGR	Q26604 schistosoma P03541 pichinde ar	P04935 lassa virus P40694 mus musculu	P38305 saccharomyc P48671 carassius a	P35014 galdieria s P02543 sus scrofa	P35567 xenopus lae P24033 xenopus lae	Q9w739 rana dybows	
884 993 1025 1025 1025 1025 1033 1033 1033 1035 1035 1035 1035 103	SMX5_SCHMA NCAP_PIARV	NCAP_LASSG SMB2_MOUSE	YB44_YEAST VIM1_CARAU	RR2_GALSU VIME_PIG	CC21_XENLA CC22_XENLA	CDC2_RANDY	THE CALGA
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ALIGNMENTS

1 RRVKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36

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MEDLINE-92380263; PubMed-1511740;
                                                TISSUE=Lung
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                                                                                                                                                                                                                                                                                                                                 Gaps
                                                           01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Carcharhinus springeri (Reef shark)
Eukaryota, Metazoa; Chordata; Cranlata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhinus;
                                                                                                                                            01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tetranectin precursor (TN) (Plasminogen-kringle 4 binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Placents;
MEDLINE-22365345; PubMed-1354271;
MEDLINE-22365345; PubMed-1354271;
Wewer U.M., Albrechtsen R.;
"Tetranectin, a plasminogen kringle 4-binding protein. Cloning and gene expression pattern in human colon cancer.";
Lab. Invest. 67:253-262(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                 DB 1; Length 166;
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                                                                                                                                                                                                                                                                                                 166 AA; 18432 MW; 53EF812DEA5C6119 CRC64;
                                                                                                                                                                                                                                                                                                           Score 124.5; DB 1;
Pred. No. 5.3e-09;
202 AA
                                                                                                                                                                                                                                                                      C-TYPE LECTIN.
                                                                                                                                                                                                                                                                                                                               6; Mismatches
                                                                                                                                                                                                                                                                                                                                              4 KEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                       | || || || || 8 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK 39
                                               166
                                                                                                                                                                                                                      InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                             PRT;
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72.7%;
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                                              STANDARD;
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25,
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(Rel. 25,
(Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                            Lectin; Cartilage.
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SEQUENCE FROM N.A.
                                                                                                                        NCBI_TaxID=7809;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1993
15-JUN-2002
                                              TETN CARSP
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                                                                                                                                      SEQUENCE
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                                      TETN_CARSP
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-!- FUNCTION: Tetranectin binds to plasminogen and to isolated kringle.
4. May be involved in the packaging of molecules destined for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE-97398360; PubMed-9226258;
MicLisen B.B. Kastrup J.S., Rasmussen H., Holtet T.L., Graversen J.H.,
Etzerodt M., Thoegersen H.C., Larsen I.K.;
"Crystal structure of tetranectin, a trimeric plasminogen-binding
protein with an alpha-helical coiled coil.";
FEBS Lett. 412:388-396(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Plasma;
MEDLINE-20080486; PubMed-10614823;
Jaquinod M., Holtet T.L., Etzerodt M., Clemmensen I., Thoegersen H.C.,
Roepstorff P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.H.,
Berglund L., Petersen T.E.;
"The gene structure of tetranectin, a plasminogen binding protein.";
FEBS Lett. 309:15-19(1992).
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-88107595; PubMed-3427041; Euhlendorff J., Clemmensen I., Magnusson S.; Fuhlendorff J., Clemmensen I., Magnusson S.; Fuhlendorff J., Clemmensen I., Magnusson S.; Furcture of tetranectin, a plasminogen kringle 4 binding plasma protein: homology with asialoglycoprotein receptors and cartilage proteoglycan core protein."; Biochemistry 26:6757-6764(1987).
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MEDLINE-98437604; PubMed=9757090;
MEASTURD J.S., Nielsen B.B., Rasmussen H., Holtet T.L., Graversen J. Etzerodt M., Thoegersen H.C., Larsen I.K.;
"Structure of the C-type lectin carbohydrate recognition domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: Secreted.
-1- MASS SPECTROMETRY: MW-20535.8; MW_ERR-2.4; METHOD-Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mass spectrometric characterisation of post-translational modification and genetic variation in human tetranectin."; Biol. Chem. 380:1307-1314(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sorensen C.B., Berglund L., Petersen T.E.; "Cloning and mapping of the murine tetranectin gene."; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE, MASS SPECTROMETRY, AND VARIANT GLY-106.
                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 22-202, AND VARIANTS SER-55 AND MET-58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, X70910, CAA50265.1, -.
EMBL, X70911, CAA50265.1, JOINED.
EMBL, X70912, CAA50265.1, JOINED.
EMBL, X64559, CAA45860.1; -.
EMBL, BC011024; AAH11024.1; -.
EMBL, X98121, CAA66803.1; -.
PIR, S42944; A29747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-36 FROM N.A.
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                                                                                                                                                                   SEQUENCE FROM N.A.
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SUBUNIT: Homotrimer (By similarity).
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-!- FUNCTION: Tetranectin binds to plasminogen and to isolated kringle
4. May be involved in the packaging of molecules, destined for
exocytosis (By similarity).
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Tetranectin precursor (TN) (Plasminogen-kringle 4 binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ibaraki K., Kozak C.A., Wewer U.M., Albrechtsen R., Young M.F.; "Mouse tetranectin: cDNA sequence, tissue-specific expression, and chromosomal mapping."; Mamm. Genome 6:693-696(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BALB/C; TISSUE-Liver; MEDLINE-98072445; PubMed-9409787; Soerensen C.B., Berglund L., Petersen T.E.; "Cloning of the murine tetranectin gene and 5'-flanking region.";
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                       Lectin; Plasma; Signal; Polymorphism; Glycoprotein; 3D-structure. SIGNAL
                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                          Score 79; DB 1; Length 202; Pred. No. 0.004;
                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                               /FTId=VAR_012318.
2B0DCB5DF22E1AB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6 X CBA; TISSUE-Lung;
MEDLINE-95137396; Pubmed-7835708;
Soerensen C.B., Berglund L., Petersen T.E.;
"Cloning of a CDNA encoding murine tetranectin.";
Gene 152:243-245(1995).
                                                                                                                                                          O-LINKED (GALNAC.
                                                                                                                                                                          /FTId=VAR_004189
                                                                                                                                                                                             /FTId=VAR_004190.
                                                                                                                                                                                                                                                                                                                                             202 AA
                                                                                                            TETRANECTIN.
C-TYPE LECTIN.
                                                                                                                                                                                                                                                           7; Mismatches
                                          InterPro: IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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G.
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                                                                                                                                                                                                                                          Query Match 43.2%;
Best Local Similarity 57.1%;
Matches 16; Conservative
                                                                                                                                                                                                                        202 AA; 22567
                                                                                                                                                                                                                                                                                                                                            STANDARD;
PIR; S24126; S24126.
PDB; 1HTN; 03-DEC-97.
PDB; 1TN3; 06-MAY-98.
Genew; HGNC:11891; TNA.
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202
198
198
197
189
25
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77
71
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                                    MIM; 187520;
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DISULFID
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                                                                                                                                                                                    VARIANT
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01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Heat shock factor protein 2 (HSF 2) (Heat shock transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN LUNG AND SKELETAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 202;
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BY SIMILARITY.

BY SIMILARITY.

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LT -> VI (IN REF. 2).

A -> T (IN REF. 2).

A -> R (IN REF. 2).

B -> Q (IN REF. 2).

B -> Q (IN REF. 2).
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                                                      -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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Pred. No. 0.0096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       517 AA
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InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Plasma; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 ELKNRMDVLAQEVALLKEKQALQTVCLK 73
SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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22257 MW;
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ilarity 57.1%;
Conservative
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202 AA;
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es 16; Conserv
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P38533;
                                  MUSCLE
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DISULFID
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MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YNI6_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                               R HSSF,

R TRANSFAC; T00972;

R TRANSFAC; T00972;

R MGD; MGI:96239; H8f2.

R MGD; MGI:96239; H8f2.

R MGD; MGI:96234; H8f2.

R InterPro; IPR000234; HSF_ETS.

B FARNTS; PR00044; HSF_DNA_bind; 1.

R PRINTS; PR00056; HSFDOMAIN; 1.

B ROSITE; PS00434; HSF_DNA_bind; 1.

R PROSITE; PS00434; HSF_DNA_LING; 1.

R M Transcription regulation; Nuclear protein; DNA-binding; Activator; KW Transcription; Heat shock; Multigene family.

FT DNA_BIND

TOWAIN 119 HSP SHORPHOBIC REPEAT HR-A/B.

TOWAIN 119 HSPROPHOBIC REPEAT HR-C.

AGR465BBCDF4EIBO CRC64;
           SUBUNIT: DNA-BINDING HOMOTRIMER IN STRESSED OR HEAT SHOCKED CELLS, OTHERWISE FOUND AS A HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC DURING NORMAL GROWTH AND MOVES TO THE NUCLEUS UPON ACTIVATION.
SIMILARITY: BELONGS TO THE HSF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                **Sheldon L., Kingston R.E.; **
"Hydrophobic coiled-coil domains regulate the subcellular localization of human heat shock factor 2."; **
Genes Dev. 7:1149-1558(1993).
--- FUNCTION: DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT SHOCK PROMOTER ELEMENTS (HSE) AND ACTIVATES TRANSCRIPTION. IN HIGHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Heat shock factor protein 2 (HSF 2) (Heat shock transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 65-71.
MEDLINE-91334377; PubMed=1871106;
Schuetz T.1., Gallo G.J., Sheldon L., Tempst P., Kingston R.E.;
"Isolation of a CDNA for HSF2: evidence for two heat shock factor genes in humans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutèleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.7%; Score 58; DB 1; Length 517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 88:6911-6915(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :: :||:: | ||:||: |: | 1| :|
143 IESRLSELKSENESLWKEVSELRAKHAQQQQVIR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.4%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION, AND MUTAGENESIS.
MEDLINE-93339580; PubMed-8339932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last seq.
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                  EMBL; X61754; CAA43893.1; -. PIR; B40583. B40583. HSSP; P22121; 2HTS. TRANSFAC; T00972; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 32.4 les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2) (HSTF 2).
HSF2 OR HSTF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSF2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSF2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                      SUBUNIT: DNA-BINDING HOMOTRIMER IN STRESSED OR HEAT SHOCKED CELLS,
EUKARYOTES, HSF IS UNABLE TO BIND TO THE HSE UNLESS THE CELLS ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R->G: FAIL TO TRANSLOCATE TO NUCLEUS.
RKR->ASS: FAIL TO TRANSLOCATE TO NUCLEUS.
00DFD05CFD9DF0D3 CRC64;
                                                                                OTHERWISE FOUND AS A HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYDROPHOBIC REPEAT HR-A/B.
HYDROPHOBIC REPEAT HR-C.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=5288C / FY1679;
MEDLINE=9610628; PubMed=8740422;
SOJet-Mira A., Salz J.E., Ballesta J.P.G., Remacha M.;
The sequence of a 17,933 bp segment of Saccharomyces cerevisiae chromosome XIV contains the RHO2, TOP2, MKT1 and END3 genes and five new open reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation; Nuclear protein; DNA-binding; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FFB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical 11.5 kDa protein in TOP2-MKT1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation; Heat shock; Multigene family.
DNA_BIND 7 112 BY SIMILARITY.
DOMAIN 119 192 HYDROPHOBIC REPEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :: : :||:: | ||:||: |: | 113 | 1143 IESRLSELKSENESLWKEVSELRAKHAQQQQVIR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Mismatches
                                                                                                                                                                -! - SIMILARITY: BELONGS TO THE HSF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 VKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.7%; Score 58; 32.4%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000232; HSF_DNA_bind.
InterPro; IPR00241; HSF_ETS.
Pfam: PP00447; HSF_DNA-bind; 1.
PRINTS; PR00056; HSFDOMAIN.
PRODOM: PD001788; HSF_DNA_bind; 1.
SMART; SM00415; HSF_1 1.
PROSITE; PS00434; HSF_LOMAIN; 1.
                                                                                                                                      TO THE NUCLEUS UPON ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60348 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M65217; AAA36017.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, P22813; 1HKT.
TRANSFAC; T01043; -.
Genew; HGNC:5225; HSF2.
MIM; 140581; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A41138; A41138.
HSSP; P22813; 1HKT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360
108
195
170
109
536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1996 (Rel. 01-FEB-1996 (Rel
                            HEAT SHOCKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YNLO86W OR N2254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YNI6_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND TESTIS, MODERATE IN HEART, SPLEEN, AND KIDNEY, AND LOW IN OTHER TISSUES.
SIMILARITY: BELONGS TO THE DNA2/NAM7 HELICASE FAMILY.
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
10-MAP-2000 (Rel. 39, Last annotation update)
(SMUBP-2) (Insulin II gene enhancer-binding protein) (RIPE3B-binding complex 3B2 P110 subunit) (RIP-1).
IGHMBP2 OR SMUBP2 OR RIP1.
Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: COMPOSED OF AT LEAST THREE POLYPEPTIDES: P58, P62, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shieh S. Y., Stellrecht C.M.M., Tsai M.-J.; Molecular characterization of the rat insulin enhancer-binding complex 3b2. Cloning of a binding factor with putative helicase
                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 270:21503-21508(1995).
-!- FUNCTION: BINDS TO THE INSULIN II GENE RIPE3B ENHANCER
                                                                                                                                                                                            29.5%; Score 54; DB 1; Length 102; 40.7%; Pred. No. 2.8;
                                                                                                                                                                                                                          9; Indels
                                                                                                        EMBL; X89016; CAA61424.1; -.
EMBL; Z71362; CAA95962.1; -.
SGD; S0005030; YRL086W.
SPPOCHELCIAL protein.
SEQUENCE 102 AA; 11461 MW; 33200D2F0F729DA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                 989 AA.
                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001374; R3H.
InterPro; IPR00058; Znf_AN1.
InterPro; IPR004483; put_DNA_helic.
Pfam; PF01424; R3H; 1.
SMATT; SM00393; R3H; 1.
SMART; SM00154; ZnF_AN1; 1.
TIGRFAMS; TIGR00376; put_DNA_helic; 1.
                                                                                                                                                                                                                                                  10 LKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                  24 LSTDLDGLYQSINELRESQALLIEMLR 50
                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95394901; PubMed=7665561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L15625; AAB00104.1; -.
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Insulinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mesocricetus
                                                                                                                                                                                                                                                                                                                                              SMB2_MESAU
Q60560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGION.
                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                   SMB2_MESAU
                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                      RESULT 8
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                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                       NUCLEAR LOCALIZATION SIGNAE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Last Sequence update)
15-VUN-2002 (Rel. 41, Last annotation update)
Keratin, type II cytoskeletal 8 (Cytokeratin 8) (Cytokeratin endo A).
KRT8 OR KRT2-8.
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89121483; PubMed-2464527;
Morita T., Tondella M.L.C., Takemoto Y., Hashido K., Ichinose Y., Nozaki M., Matsushiro A.
Nozaki M., Matsushiro A.
"Nucleotide sequence of mouse Endoa cytokeratin cDNA reveals
"Outpeptide characteristics of the type-II keratin subfamily.";
Gene 68:109-117(1988).
-i- SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-88255624; PubMed-2454862; Semat A., Vasseur M., Maillet L., Brulet P., Darmon Y.M.; "Sequence analysis of murine cytokeratin endo A (no. 8) cDNA. Evidence for mRNA species initiated upstream of the normal 5' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KERATIN 8 ASSOCIATES WITH KERATIN 18.

-!- MISCELLANBOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND MICROFIBRILLAR KERATIN, I (ACIDIC) AND II (NEUTRAL TO BASIC) (40-55 AND 56-70 KILODALTONS, RESPECTIVELY).

-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                          SS DNA-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                               Length 989;
                                                                                                                                                                                                                                                                                                                                    Indels
ATP-binding; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                 DB 1;
                                       ATP · (POTENTIAL).
LEU-RICH.
                                                                                                                                                                                                                                                            28.7%; Scur.
35.5%; Pred. No. 52,
... 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   488 AA
                                                                                                                                                  GLN/PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                 5 EKDGDLKTQVEKLWREVNALKEMQALQTVCL 35
                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-VAL.
                                                                                                                                                                               POLY-LYS.
                          Transcription regulation; Activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, X12789; CAA31278.1; -.
EMBL, X15662; CAA33597.1; -.
EMBL, M21836; AAA37550.1; -.
EMBL, M21836; AAA37551.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S05474; S05474.
SWISS-2DPAGE; P11679; MOUSE.
MGD; MGI:96705; KTt2-8.
InterPro; IPR001664; IF.
InterPro; IPR003054; Keratin_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Differentiation 37:40-46(1988).
                                                                                                                                                                                                                               108439 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1989 (Rel. 12, Created)
01-NOV-1997 (Rel. 35, Last seq
                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                          425
373
783
859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                            989 AA;
                                                                                                                                                                                                                                                                                                         Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                               213
250
370
637
793
860
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P11679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells
                                             NP_BIND
DOMAIN
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DNA_BIND
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                    Aatches
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34

3 VKEKDGDLKTQVEKLWREVNALKEMQALQTVC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY MAPK AND CAMK2) (BY
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanothermaceae; Methanothermus.
                                                                                                                                                                                                                                             Score 52; DB 1; Length 488; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.9%; Score 51; DB 1; Length 131; 31.2%; Pred. No. 9; ive 10; Mismatches 12; Indels
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                             -> R (IN REF. 2).
9E1430800BB81523 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 AA; 15086 MW; B7C6F746AB0C98AF CRC64;
                                                                                                                                                                                                   -> EA (IN REF. 2).
                                                                                                                                                                                         OO -> NR (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Methyl-coenzyme M reductase operon protein D.
                                                                                                                                                                                                                                                                                                                                                                 131 AA
                                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                            SIMILARITY)
                                                                                                                                                                                                                                                                                                    300 KHGDDLRRTKTEISEMNRNINRLQEIEALK 329
                                                                                        COIL 1A.
LINKER 1.
COIL 1B.
                                                                                                                         LINKER 12.
                                                                                                                                                                                                                                                                                     6 KDGD----LKTQVEKLWREVNALKEMQALQ 31
                                                                                                                                   COIL 2.
STUTTER.
                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                         HEAD.
Pfam; PF00038; filament; 1.
PRINTS; PR01276; TYPE2KERATIN.
PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003901; MthcoMR_D. Pfam; PF02505; MCR_D; 1. Methanogenesis.
                                                                                                                                                                                                                        54318 MW;
                                                                                                                                                                                                                                             28.4%;
36.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 31.28
Marches 10; Conservative
                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J03375; AAA72194.1;
                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanothermus fervidus.
                                                                                                              240
264
402
346
23
436
                                                                                                                                                                                     189
324
366
488 AA;
                                                                                                                                                                                                                                                      Similarity
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P12974;
                                             INIT_MET
DOMAIN
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PP2A, subunit B', PR53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete sequence and conserved synteny groups confirm its common ancestry with red algae.";
J. Mol. Evol. 48:236-244(1999).
-! SIMILARITY: BELONGS TO THE S2P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=99128221; Pubmed=9929392;
Douglas S.E., Penny S.L.;
"The plastid genome of the cryptophyte alga, Guillardia theta:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.9%; Score 51; DB 1; Length 235; 37.0%; Pred. No. 17; 1.ive 8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTPA_HUMAN STANDARD, PRT; 358 AA. 01528; Q1528; Q1528; Q9BUKL; Q9NNZ7; Q9NNZ8; Q9NNZ9; L15-JUN-2002 (Rel. 41, Created) L15-JUN-2002 (Rel. 41, Last sequence update) L15-JUN-2002 (Rel. 41, Last annotation update) Protein phosphatase 2A, regulatory subunit B' (PP2A, subpaper OR PTPA) (PP2A) PPP2R4 OR PTPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ribosomal protein; Chloroplast.
SEQUENCE 235 AA; 26712 MW; 1360A0A1368A6A93 CRC64;
                                                                                                                                                                                                                                                                                                                            Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
NCBI_raxID-55529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (ISOFORM 1).
                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Chloroplast 30S ribosomal protein S2.
                                                                                                                                235 AA
TIGREAMS; TIGRO1011; rpsB bact; 1.
PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
PROSITE; PS00963; RIBOSOMAL_S2_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:: |::||| |:| |:|
130 KKEAAGLRRELEKLKRNLNGIKNMKRL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 KEKDGDLKTQVEKLWREVNALKEMQAL 30
                                                                                                                                                                                                                                                                                 Guillardia theta (Cryptomonas phi).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF041468; AAC35673.1; -. InterPro; PR0014865; Ribosomal_S2. Pfam; PF00318; Ribosomal_S2; 1. PRINTS; PR00395; RIBOSOMALS2.
                                                                                                                                STANDARD;
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                        Chloroplast.
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                                                                                                       RR2_GUITH
ID RR2_GUITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                  078482;
                                                                                    RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                              AMD MG(2+) (IN VITRO).

-!- SUBUNIT: ASSOCIATES WITH PP2A HETERODIMERIC CORE ENZYME, COMPOSED OF A 36 KDA CATALYTIC SUBUNIT C) AND A 65 KDA CONSTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A).

-!- ALTERNATIVE PRODUCTS: 4 ISOFORMS: 1/ALPHA, 2/BETA (SHOWN HERE), 3/DELTA AND 4/EPSILON; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: REVERSIBLY STIMULATES THE VARIABLE PHOSPHOTYROSYL PHOSPHATASE ACTIVITY OF PP2A CORE HETERODIMER IN PRESENCE OF ATP
                                                                                                                                                 Van Hoof C., Aly M., Garcia A., Cayla X., Cassiman J., Merlevede W.,
                                                                                                                                                                                                                                                                                                "Identification and characterization of alternative splice products encoded by the human phosphotyrosyl phosphatase activator gene."; Eur. J. Biochem. 267:4406-4413(2000).
                                                                                                                                                                          "Structure and chromosomal localization of the human gene of the phosphotyrosyl phosphatase activator (PTPA) of protein phosphatase
                                                      protein that activates the tyrosyl phosphatase activity of protein
                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 4).
MEDLINE-20341117; Pubmed-10880964;
Janssens V., van Hoof C., Martens E., de Baere I., Merlevede W.,
MEDLINE-94253154; PubMed-8195217;
Cayla X., Van Hoof C., Bosch M., Waelkens E., Peeters B.,
Merlevede W., Goris J.;
"Molecular cloning, expression, and characterization of PTPA, a
                                                                   phosphatase 2A.";
J. Biol. Chem. 269:15668-15675(1994).
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                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                   Genomics 28:261-272(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAA60163.1;
CAA60163.1;
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                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X86435;
X86436;
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X86432;
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                                                                                                                        TISSUE-Blood;
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                                                                                                                                                               Goris J.;
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Gallus gallus (Chiken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83299221; PubMed-6310496;
Dahan A., Reynaud C.-A., Waill J.-C.;
Nucleotide sequence of the constant region of a chicken mu heavy
chain immunoglobulin mRNA.;
                                                                                                                                                                                                                                                                                                                                          MISSING (IN ISOFORM 3).
MISSING (IN ISOFORM 1).
MISSING (IN ISOFORM 4).
L -> V (IN REF. 2 4).
MISSING (IN REF. 2 A).
S -> V (IN REF. 1; AA SEQUENCE).
W; 6A99C521AF5F6BEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51; DB 1; Length 358; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUC_CHICK STANDARD; PRT; 446 AA. P01875; 21-JUL-1986 (Rel. 01, Created) 21-FBB-1991 (Rel. 17, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 VKEKDGDLKTQVEKLWREVNALKEMQALQTV 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004327; Phstyr_phstse_ac.
Pfam; PF033095; PPPA; 1.
Alternative splicing.
VARSPLIC 45 108 MISSING (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 11:5381-5389(1983)
                                                                   EMBL, X86439; CAB77602.1; JOINED. EMBL, X86429; CAB77603.1; -. EMBL, X86439; CAB77603.1; -. EMBL, X86439; CAB77603.1; JOINED. EMBL, X86434; CAB77603.1; JOINED. EMBL, X86435; CAB77603.1; JOINED. EMBL, X86435; CAB77603.1; JOINED. EMBL, X86438; CAB77603.1; JOINED. EMBL, X86438; CAB77603.1; JOINED. EMBL, X86438; CAB77603.1; JOINED. EMBL, X86439; CAB77603.1; JOINED. EMBL, S86439; CAB77603.1; JOINED. EMBL, S86439; CAB77603.1; JOINED. EMBL, S86439; CAB77603.1; JOINED. EMBL, S86439; CAB77603.1; JOINED. EMBL, S0002545; AAH11605.1; -.
                           JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         358 AA; 40681 MW;
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38.78;
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                           X86436; CAB77602.1;
X86437; CAB77602.1;
X86438; CAB77602.1;
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                                                                                                                                                                                                                                                               HGNC:9308; PPP2R4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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             X86435;
X86436;
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MIM; 600756;
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                             EMBL;
EMBL;
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EMBL; X01613; CAA25762.1; -.

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nucleoporins.
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P52296;
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                          PIR;
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
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SEDUENCE FROM N.A.
MEDLINE-97061201; PubMed-8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Kaneko T., Sato S., Kugiura M., Sasamoto S., Kimura T.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marthez-Perez I.M., Vioque A.;
Mucleotide sequence of the phytoene desaturase gene from
Synchocystis sp. PCC 6803 and characterization of a new mutation
which confers resistance to the herbicide norflurazon.";
Plant Mol. Biol. 18:981-983(1992).
                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                         (POTENTIAL).
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                                                                                                                                                                                                                                                                                  (POTENTIAL)
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(BY SIMILARITY)
N-LINKED (GLCNAC...) (POTENTIX
N-LINKED (GLCNAC...) (POTENTIX
N-LINKED (GLCNAC...) (POTENTIX
                                                                                                                                 C-TERMINAL REGION.
INTERCHAIN (WITH A LIGHT CHAIN)
(BY SIMILARITY).
                                                                                                                                                                           BY SIMILARITY.
INTERCHAIN (WITH A HEAVY CHAIN)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-1992 (Rel. 24, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase).
                                                                                                                                                                                                                                                                                                          DB 1; Length 446;
                                                                                                                                                                                                                                                                                                                          14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vioque A ; Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                 LINKED (GLCNAC. . .) (P. 3CBOCE108949BD17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synechocystis sp. (strain PCC 6803).
Bacteria: Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                              (GLCNAC...)
(GLCNAC...)
(GLCNAC...)
(GLCNAC...)
                                                                             Immunoglobulin C region.
                                                                                                                                                        SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                     472 AA
                                                                                                                                                                                                                                                                                                                          5; Mismatches
                                                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                    254 KEKGGKLETALGKRVLQSNGLYTVDGVATVC 284
                                                                                                                                                                                                                                                                                                          Score 51;
                                                                                                                                                                                                                                                                                                                                          4 KEKDGDLKTQVEKLWREVNALKEMQALQTVC 34
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N-LINKED (
N-LINKED (
N-LINKED (
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MEDLINE-92256820; PubMed-1581575;
      HSSP, P01857, IFC1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                        48173 MW;
                                                                                                                                                                                                                                                                                                        27.98;
38.78;
                                        Pfent, PF00047; ig; 3.
SMART; SM00410; IG_like; 2.
SMART; SM00407; IGcl; 1.
                                                                     PROSITE; PS00290; IG_MHC; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                             Immunoglobulin domain;
NON_TER 1
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190
296
284
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                                                                                                                                                                                                             445
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73
130
198
382
433
446 AA;
                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                      106
210
317
428
                                                                                                                                                        27
135
237
284
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                                                                                                                                                                                                                                                                                                                                                                                                    CRTI_SYNY3
P29273;
                                                                                                                                                                 DISULFID
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CARBOHYD
CARBOHYD
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                          Matches
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Hosouchl T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yasuda M., Tabata S., Saquence analysis of the genome of assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).

-I- FUNCTION: THIS ENZYME CONVERTS PHYTOENE INTO ZETA-CAROTENE VIA TINTERMINISTRY OF PHYTOFULENE BY THE SYMMETRICAL INTRODUCTION OF TO DOUBLE BONDS AT THE C-11 AND C-11' POSITIONS OF PHYTOENE.

-I- COPACTOR: NAD, NADD, OR FAD (PROBABLE).

-I- ENZYME REGULARION: INHIBITED BY THE HERBICIDE NORFLURAZON IN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Importin beta-1 subunit (Karyopherin beta-1 subunit) (Nuclear factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-Buffalo; TISSUB-Liver;
MEDLINE-95183547; PubMed-7878057;
Radu A., Blobel G., Moore M.M.;
"Identification of a protein complex that is required for nuclear protein import and mediates docking of import substrate to distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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-:- SUBCELLULAR LOCATION: Membrane-associated (Probable).
-:- SIMILARITY: BELONGS TO THE PHYTOENE DEHYDROGENASE FAMILY.
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36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      875 AA
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Pred. No. 3
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"Mammalian karyopherin alpha 1 beta and alpha 2 beta heterodimers: alpha 1 or alpha 2 subunit binds nuclear localization signal and beta subunit interacts with peptide repeat-containing nucleoporins."; proc. Natl. Acad. Sci. U.S.A. 92:6532-6536(1995).

-I- FUNCTION: REQUIRED FOR NUCLEAR PROTEIN IMPORT AND MEDIATES DOCKING OF IMPORY SUBSTRATE TO DISTINCT NUCLEOPORINS. SERVES A RECEPTOR FOR NUCLEAR LOCALIZATION SIGNALS.

-I- SUBUNIT: FORMS A COMPLEX WITH AN IMPORTIN ALPHA SUBUNIT.

-I- SUBURIT: BELONGS TO THE IMPORTIN BETA FAMILY.

-I- SIMILARITY: CONTAINS 1 HIPORTIN N-TERMINAL DOMAIN.

-I- SIMILARITY: CONTAINS 8 HEAT REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transport; Protein transport; Repeat; Nuclear protein.
DOMAIN 21 100 IMPORTIN N-TERMINAL.
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9CD77A05744014C4 CRC64;
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InterPro; IPR000225; Armadillo.
InterPro; IPR001357; HEAT_repeat.
InterPro; IPR011944; Importinb_N.
Pfam; PR0514; Armadillo.seg; 3.
PROSITE; PS50077; HEAT_REPEAT; 1.
PROSITE; PS50166; IMPORTIN_B_NT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEAT 3.
HEAT 4.
HEAT 5.
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97123 MW;
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Best Local Similarity 35.1
Matches 13; Conservative
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Search completed: April 15, 2003, 11:48:34 Job time : 8.5 secs

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329.675 Million cell updates/sec
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                        1 RRVKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR
                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	, Description	028008 bos taurus	O9epw4 mus musculu	09ddd4 qallus qall	013870 schizosacch	O9cr92 musculu	09x082 thermotoga	O9n4m4 caenorhabdi	Q8ued7 agrobacteri	Q9cwr2 musculu	Q9bs48 homo sapien	Q9r120 rattus norv	Q8vej0 mus musculu	Q9z218 mus musculu	Q98qp5 mycoplasma	, 096qw4 homo sapien	Q96ai5 homo sapien
SUMMARIES	ΩI	Q28008	Q9EPW4	Q9DDD4	013870	Q9CR92	09x082	Q9N4M4	Q8UED7	Q9CWR2	Q9BS48	Q9R120	Q8VEJ0	09Z2L8	Q98QP5	Q96QW4	Q96AI5
	DB	9	11	13	m	11	16	ß	16	11	4	11	11	11	16	4	4
	Length DB	197	196	201	630	584	1008	7659	251	428	230	513	517	535	631	171	239
dР	Query Match	100.0	7.06	46.7	35.5	33.9	33.3	33.3	32.2	32.0	31.7	31.7	31.7	31.7	31.7	31.4	31.4
	Score	183	166	85.5	65	62	61	61	59	58.5	58	58	28	58	28	57.5	57.5
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QY Db

09h7b4 homo sapien 096m63 homo sapien 09h8a7 homo sapien p97690 rattus norv 060464 homo sapien 097594 bos taurus 097544 bos taurus 09p2k1 homo sapien 027806 methanobact 02425 ganoderma 1 099113 arabidoosis	Q92424 ganoderma 1 Q9kea0 bacillus ha Q27097 methanobact Q8zay8 yersinia pe Q9mth5 cenothera h Q9p4v6 candida boi Q9beb1 neurospora	Q18406 caenorhabdi Q25761 helicobacte Q23077 arabidopsis Q96ek2 homo sapien Q96ek2 homo sapien Q95k70 arabidopsis Q9382 neurospora Q9382 neurospora Q9442 ganoderma f Q9944 leishmania	Q9utr7 schizosacch
4 4 4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		659 5 759 16 319 10 531 4 862 10 976 10 1011 3 142 3 455 5	952 3 0
57.5 57.5 57 57 57 57 57 58 58 58	5 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	იი იიი 44 ნ. გ.	53.5
118 118 119 120 122 123 124 125 126	3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	24444433333 244444433344444444444444444	45

ALIGNMENTS

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Gaps
                                                                                                           C-type lectin homolog precursor.

C-type lectin homolog precursor.

Eukaryota; (Bovine).

Busaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovinae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 197;
                                                                                                                                                                                                                                                              Neame P.J., Boynton R.E.;

"C-type lectin homolog from bovine cartilage.";

"C-type lectin homolog from bovine cartilage.";

Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

R EMBL, 022298; AAC18614.1;

R HSSP: P05452; 1TN3.

R InterPro; 1PR001304; Lectin_C.

R Pfam; PF00059; lectin_C; 1.

R SMART; SM00034; CLECT; 1.

R PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.

R PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL 1 24 POTENTIAL.
CHAIN 25 197 C-TYPE LECTIN HOMOLOG.
SEQUENCE 197 AA; 22215 MW; AAAC4280F41ACOF4 CRC64;
                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 183; DB 6;
100.0%; Pred. No. 6.6e-16;
tive 0; Mismatches 0;
                                197 AA
                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                PRELIMINARY;
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=CARTILAGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                NCBI_TaxID=9913;
                               928008
RESULT 1
Q28008
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9CR92;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                               STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                 013870 013870;
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            RESULT 4
013870
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09CR92
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                                                                                                                                                                                                                                                                                          Neame P.J., Grimm D.R.;
"Mouse homolog of human CLECSFI, a cartilage derived C-type lectin.";
"Mouse homolog of human CLECSFI, a cartilage derived C-type lectin.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
HSSP, P05462; 1HTM.
InterPro, 1PR001304; Lectin.C.
Pfam; PF00059; lectin.C.
SMART, SM0034; CLECT: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauría; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 196;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "West of the chicken.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
BMBL, A1277116; CAC20217.1; -.
HSSP: P05452; 1TM3.
InterPro; IPR001304; Lectin_C.
Fram; PR00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 201 AA; 22172 MW; 7C7F235D24426AE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 196 AA; 22191 MW; 9AE4C809D119E852 CRC64;
                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
C-type lectin superfamily 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 90.7%; Score 166; DB 11; Similarity 91.7%; Pred. No. 1e-13; 33; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.7%; Score 85.5; DB 13;
48.7%; Pred. No. 0.0027;
live 6; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 EKDG-----DLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RRVKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS500615; C_TYPE_LECTIN_1; 1. PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                           PRT;
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                                         PRELIMINARY;
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les 19; Conserv
                                                                                                                                                                                                                                                                         STRAIN-ES129/SV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tetranectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Best Local 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                       Q9EPW4
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RESULT 2
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                    Q9EPW4
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TISSUE—TESTIS;

X MEDLINE—21085660, Dubmed—11217851;

XA Atzawa K., Tawa M., Shibata K., Yoshino M., Itch M., Ishil Y.,

RA Atzawa K., Tawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Atzawa K., Tawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Atzawa K., Tawa M., Ashburner M., Baralov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Brownstein M.J., Bult C., Fletcher C., Fullia M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodilguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RY Winshaw-Boris A., Yoshida K., Rawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murphy L., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: TO YEAST NOT3.
EMBL; 298598; CAB11234.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.5%; Score 65; DB 3; Length 630; 43.2%; Pred. No. 3.9; Live 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-ALA.
POLY-ASP.
4 4F9284439845CB71 CRC64;
                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                           01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 06, Last annotation update)
Probable transcriptional regulator CLB3.05.
SPACIB3.05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 KEK-DGDLKTQVEKL-----WREVNALKEMQAL 30
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POLY-SER.
   PRT;
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PRELIMINARY;
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4921513E08RIK
                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces.
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Matches 16; Conserv
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8UED7
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                                                                                                                                                                                                                                                                                                                                                                                                                     Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
HoDonald L., Ulterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Mature 399:323-329(1999).
TIGR: TM0987;
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                 Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga
          "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.3%; Score 61; DB 16; Length 1008; 43.8%; Pred. No. 21; ive 4; Mismatches 8; Indels
                                                                                                 Score 62, DB 11; Length 584;
Pred. No. 8.8;
9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4D640F610123E614 CRC64;
                                 EMBL; AKO15646; BAB29914.1; -.
EMBL; AKO14878; BAB29599.1; -.
MGD; MGI:1913967; 4921513E08Rik.
SEQUENCE 584 AA; 67255 MW; 0F360DF474D78E18 CRC64;
                                                                                                                                                                                                                                                                                   12, Last sequence update)
20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 7659 AA.
                                                                                                                                                                                                                                              PRT; 1008 AA
                                                                                                                                                                1 RRVKEKDGDLKTQVEKLWREVNALKEMQALQTV 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 KVKVKDGDLIFEPATKEDSEKLWKAKEKVREM 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RVKEKDGDL-----KTQVEKLWREVNALKEM 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002052; NG_Mtase.
PROSTTE; PS00092; NG_MTARE; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 1008 AA; 115760 MW; 4D640Ff
                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-MSBB / DSM 3109;
MEDLINE-99287316; Pubmed=10360571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical 854.0 kDa protein.
                                                                                                   33.9%;
36.4%;
                                                                                                                                                                                                                                                                                 (TrEMBLrel. 12, (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                          Hypothetical protein TM0987
                                                                                                                            12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                 01-NOV-1999
                                                                                                                                                                                                                                                                                              01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9N4M4;
                                                                                                                                                                                                                                                         Q9X082
                                                                                                                                                                                                                                           Q9X082
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Matches
                                                                                                                                                                                                                  RESULT 6
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genome of the natural genetic engineer Agrobacterium tumefaciens
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MEDLINE-2160851; PubMed-11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Goodner B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21608550; PubMed-11743193; Mooks D.E., Kitajima J.P., Mood D.W., Setubal J.C., Kaul R., Mooks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ABC transporter, nuclectide binding/ATPase protein.
SUFC OR ATU1823 OR AGR_C_3346.
Bachoacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizoblaceae group;
                                                                                          "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston R.;
"Direct Submission.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006834; AAF40010.2; -
InterPro; IPR001092; HLH_basic.
SMART; SM00264; BAG; 1.
PROSITE; PRO01038; HELIX_LOOP_HELIX; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 7659 AA; 854006 MW; BBB95964D79B4FFI CRC64;
                                                                                                                                                                                                                                                                                                            Gattung S., Goela D., Broy M.;
"The sequence of C. elegans cosmid ZK973.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.3%; Score 61; DB 5; Le
45.7%; Pred. No. 1.7e+02;
iive 7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 VKEKDGDLKTQVEKLWREV----NALKEMQALQTV 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 45.7
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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RESULT 10

pathogen and biotechnology agent

"Genome sequence of the plant parchacterium tumefaciens C58."

Agrobacterium tumefaciens

RT RL DR DR SQ SQ

09CWR2; Q9CWR2

RESULT 9 Q9CWR2

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WEDURDE FROM N.A.

WEDLINB-20571092: PubMed-11121583;

An IN. Han M.Y., Lee S.S., Kilm K.J., Park Y.M.;

MIN J.N., Han M.Y., Lee S.S., Kilm K.J., Park Y.M.;

An In. Heat shock factor 2 expression during the early canogenic phase of embryogenesis.";

EMBL: AF172640; AAD51329.1;

EMBL: AF172640; AAD51329.1;

RESPONDED IPRO00232; HSF_DNA_bind.

InterPro: IPRO02341; HSF_DNA_bind.

PRINTS: PRO0045, HSF_DNA_bind.

PRINTS: PRO0045; HSF_DNA_bind.

PRODOM: PD001788; HSF_DNA_bind; 1.

PRODOM: PD001788; HSF_DNA_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                Homo sapiens (Human).

Belaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NGBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                A Strausberg R.;
L Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC005329; AAH05329.1;
R FMSP: P22813; LHT.
R InterPro; IPR00232; HSF_DNA_bind.
R InterPro; IPR00232; HSF_DNA_bind.
R InterPro; IPR00561; HSF_DNA_bind.
R RINTS; PR0047; HSF_DNA_bind; 1.
R RINTS; PR00056; HSF_DNA_bind; 1.
R PRINTS; PR0001788; HSF_DNA_bind; 1.
SMART; SM00415; HSF, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.7%; Score 58; DB 4; Length 230; 32.4%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 AA; 27027 MW; 01C72FAA9E62D37A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00434; HSF_DOMAIN; 1.
SECHIFNCE 513 AA; 57743 MW; 55DB2DC250B13BB5 CRC64;
                                                                                      01-JUN-2001 (TrEWBLrel. 17, Created)
01-JUN-2001 (TrEWBLrel. 17, Last sequence update)
01-DEC-2001 (TrEWBLrel. 19, Last annotation update)
Similar to heat shock transcription factor 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                    230 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          513 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY 2000 (TrEMBLrel. 13, 01-MAY 2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19, Heat shock factor 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 32.4%
Matches 11; Conservative
                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      TISSUE=BLADDER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heat shock.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09R120;
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                       Q9BS48
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RX MEDLINE-21085660; PubMed-11217851;

RA ARAWA T., Shingawa A., Shibata K., Yoshino. M., Itoh M., Ishii Y.,

RA Arawa T., Shingawa A., Shibata K., Yoshino. M., Itoh M., Ishii Y.,

RA Arawa K., Izawa M., Nishi K., Konoo H., Adachi J., Fukuda S.,

RA Aito T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Cuackenbush J.,

RA Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schrim L.M., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fullita M., Wagner L.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Sasaki H., Sato B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wunshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                   Query Match 32.2%; Score 59; DB 16; Length 251; Best Local Similarity 41.5%; Pred. No. 9; Matches 17; Conservative 3; Mismatches 15; Indels
                                                                                                                                                                                          Indels
                                                                                      251 AA; 27290 MW; 30CB7C61B337B98D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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49126 MW; 1EC765044E1FB0DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                      1 RRVKEKDGDLKTQVEKLWREVNA-----LKEMQALQTVCL 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : ::|| |: | |::|:|| :||:|| 267 QTQDKDADMLTGDEQIWKEVQESLKKIEELK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RVKEKDGDLKTQVEKLWREV-NALKEMQALQ 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                     EMBL, AE009136; AAL42819.1; --
EMBL, AE008102; AAK87592.1; --
Complete proteome.
SEQUENCE 251 AA; 27290 MW;
Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2002 (TrEMBLrel. 21, 2410008A19R1k protein.
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                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fam; PF00856; SET; 1. -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Gaps

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13; Indels

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Indels

13;

Length 513;

SEQUENCE PROSITE;

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MEDLINE=21267165; PubMed=11353084; Chambaud I., Hellig R., Ferris S., Barbe V., Samson D., Galisson F., Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C., Blanchard A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma pulmonis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.7%; Score 58; DB 16; Length 631; 52.4%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                       Length 535;
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                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                             PROSITE; PS00434; HSF_DOMAIN; 1.
SEQUENCE 535 AA; 60224 MW; 47972520402ABB13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
SEQUENCE 631 AA; 73165 MW; 2D70547C6BC5C395 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                      Query Match 31.7%; Score 58; DB 11; Best Local Similarity 32.4%; Pred. No. 27; Matches 11; Conservative 10; Mismatches 13
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                                                                                                                                                                                                                                                                                                                                                                                             3 VKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 29;2145-2153(2001).
EMBL: AL445564; CAC13489.1; -.
MypuList; MYPU_3160; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                      JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                       JOINED.
JOINED.
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                                                                   JOINED
                                                                                JOINED
                                                                                            JOINED
                                                                                                            JOINED
                                                                                                                                                                                         InterPro; IPR000232; HSF_DNa_bind.
InterPro; IPR002341; HSF_ETS.
Pfam; PF00447; HSF_DNA-bind; 1.
PRINTS; PR00156; HSF_DNA_bind; 1.
ProDom; PD001788; HSF_DNA_bind; 1.
SMART; SM00415; HSF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasmataceae; Mycoplasma
                        AAD02417.1;
AAD02417.1;
                                                                AAD02417.1;
AAD02417.1;
                                                                                            AAD02417.1;
AAD02417.1;
                                                                                                                       AAD02417.1;
AAD02417.1;
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                                                   AAD02417.1;
                                                                                                                                                   AAD02417.1;
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                                                                                                                                                                              Hsf2.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2107;
                                                                              AF045621;
                                                                                             AF045622;
                                                                                                                       AF045624;
                                                                                                                                      AF045625;
                        AF045617;
                                      AF045618;
                                                    AF045619;
                                                                                                                                                     AF045626;
                                                                                                                                                                               MGD; MGI:96239;
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Q96QW4;
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                                                                                             EMBL;
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                                                                                                                                     EMBL;
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EMBL: AF045627; AAD02417.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sarge K.D., Zimarino V., Holm K., Wu C., Morimoto R.I.;
Cloning and characterization of two mouse heat shock factors with
distinct inducible and constitutive DNA-binding ability.";
Genes Dev. 5:1902-1911(1991).
                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                        Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC018414; AAH18414.1; -. MGD; MGI:96239; Hsf2.
                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00434; HSF_DOMAIN; UNKNOWN_1.
SEQUENCE 517 AA; 58168 MW; E5D5695B31DF3A06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
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                                                                                                         517 AA.
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                           :: : :||:: | ||:||: | :| 13
143 IESRLSELKSENESLWKEVSELRAKHAQQQQVIR 176
          3 VKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
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                                                                                                                                     Created)
                                                                                                          PRT;
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ProDom; PD001788; HSF_DNA_bind; 1.
SMART; SM00415; HSF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000232; HSF_DNA_bind.
InterPro; IPR002341; HSF_ETS.
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MEDLINE=92009180; PubMed=1717345;
                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00447; HSF_DNA-bind; 1.
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21,
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                                                                                                         PRELIMINARY;
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01-JUN-2002 (TrEMBLrel.
Heat shock factor 2.
                                                                                                                                  01-MAR-2002 (TrEMBLrel.
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01-MAY-1999 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Gaps

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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE BA74P14.1 (Novel protein) (Fragment).
OS Homo saplens (Human).
OC EUKATYOTA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NOSI-TaxID-9606;
RN 1]
RP SEQUENCE FROM N.A.
RA Cobley V.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR Nobley V.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR TherePro: IPRO01214; SET.
DR TherePro: IPRO01214; SET.
DR Pfan: PF00856; SET; 1.
PROSITE; PS50280; SET; 1.
PROSITE; P
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Search completed: April 15, 2003, 11:50:14 Job time: 25.5 secs

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Protein encoded by	Human breast tumou	Membrane-bound pro	. Human PRO polypept	Human PRO1345 (UNO	. Human tumour-assoc.	H6FXTN23 fusion pr	Human tetranectin	H6FXTN123 fusion p.	Human tetranectin.
, DI	AAB28526	AAU82642	AAY66756	AAU29161	AAB65279	AAE20465	AAW94264	AAW94256	AAW94262	AAR60521
DB	21	23	21	22	22	23	20	20	20	15
å Query Match Length DB	197	197	206	206	206	206	180	181	197	202
% Ouery Match	61.4	61.4	61.4	61.4	61.4	61.4	45.4	45.4	45.4	45.4
Score	113.5	113.5	113.5	113.5	113.5	113.5	84	84	84	84
Result No.	Т	7	e	₹	2	9	7	æ	6	10

A novel isolated polypeptide comprising an immunogenic portion of a breast cancer protein useful in the detection and treatment of breast

Human EST encoded CIIH6FXTN123 fusio Sequence of Chain Tetranectin polype H6FXtripa fusion p H6FXtripa fusion p H6FXtripb fusion p H6FXtripb = UB fusion p H6FXtripBa-UB fusion p H6FXtripBa-UB fusion p H6FXtripBa-CFV(CEA6) lrip Breast and ovarian H8F. Home sapiens Sequence encoded b Human heat shock t GFP-H8F1 fusion pr Bs]I methylase. B Human colon cancer putative p. abyssi Drosophila melanog Human polypeptide Huntingtin interac Lung small cell ca Human polypeptide Human huntingtin interac Human huntingtin interac	Artificial recogni Amino acid sequenc Drosophila melanog Human protein sequ Novel human diagno
AAW24034 AAW94251 AAW94254 AAW94255 AAW94255 AAW94255 AAW94266 AAW94266 AAW94266 AAW94266 AAW94266 AAW94269 AAW94269 AAW5033 AAY5948 AAW5033 AAY59268 AAW5033 AAY59268 AAW5033 AAY59268 AAW6029 AAW6029 AAW6039	
222 222 222 222 222 202 232 203 203 204 203 204 204 204 204 204 204 204 204 204 204	
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1.111111111111111111111111111111111111	

ALIGNMENTS

AAB28526 ID AAB	AAB28526 standard; Protein; 197 AA.
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AC.	AAB28526;
X E	07-ppp-3001 (first outre)
: X	
DE	Protein encoded by human breast tumour cDNA clone B532S.
××	
ΚW	Human; breast tumour antigen; cytostatic; immunotherapy;
Κ¥	breast cancer; vaccine.
×	
so	Homo sapiens.
XX	
PN	WO200061756-A2.
×	
PD	19-0CT-2000.
×	
PF	10-APR-2000; 2000WO-US09688.
×	
PR	09-APR-1999; 99US-0288950.
PR	02-JUL-1999; 99US-0346327.
XX	
PA	(CORI-) CORIXA CORP.
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Ιď	Reed SG, . Xu J, Dillon DC;
XX	
DR	WPI; 2000-638568/61.
DR	N-PSDB; AAC79471.
×	
ΡŢ	isolated polypeptide
ΡŢ	breast cancer protein useful in the detection and treatme

⁽without alignments)
166.853 Million cell updates/sec US-09-445-576A-39 185 1 SKSGKGKDDLRNEIDKLWREVNSLKEMQALQTVCLK 36

Scoring table:

⁹⁰⁸⁴⁷⁰ seqs, 133250620 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

⁹⁰⁸⁴⁷⁰ Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Query Match
                                                                                                                                                           RESULT 3
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              x os
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                                                                                                                    Db
                                                                                                                                                                                                                    1;
                                             The present sequence is encoded by a cDNA sequence which was isolated from a breast tumour cDNA library. It is provided in a specification relating to compounds for immunotherapy and diagnosis of breast cancer. Breast tumour antigens and the polynucleotides that encode them may be used in the production of a pharmaceutical composition to be used in the production of a proliferated T cells and incubated antigen presenting cells are also required. The polypeptides and polynucleotides may also be used to produce a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides. The sequences are useful for treating cancer, preferably breast cancer, in a patient or for stimulating an immune response. The brothucleotides and polypeptides are also useful in the diagnosis and monitoring of breast cancer. A method for detecting the presence of a cancer in a patient, comprises obtaining a biological sample from the patient, contacting the biological sample with a binding agent that binds to a breast tumnour polypeptide, detecting in the sample an amount of polypeptide that binds to the binding agent, and comparing the amount of polypeptide to a predetermined cut-off value, therefore determining the presence of a cancer in the patient. Sequences AAU82641-AAU82655 represent human breast tumour polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotides encoding breast tumour polypeptides, useful for treating breast cancer or stimulating an immune response -
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                   1;
                                                                                                                                                                                    61.4%; Score 113.5; DB 21; Length 197; 66.7%; Pred. No. 1.6e-07; 1ve 7; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to polynucleotides encoding breast tumour
                                                                                                                                                                                                                                                                                                                                                                                                                  Human; breast tumour polypeptide; breast cancer; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xu J, 'Dillon DC, Retter MW, Harlocker SL;
                                                                                                                                                                                                                                 5 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK 36
                                                                                                                                                                                                                                               Human breast tumour polypeptide clone #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 142-143; 150pp; English.
                       Claim 2; Page 90-91; 95pp; English,
                                                                                                                                                                                                                                                                                                                   AAU82642 standard; Peptide; 197 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JUN-2000; 2000US-0602877.
12-OCT-2000; 2000US-0687507.
06-FEB-2001; 2001US-0778381.
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N-PSDB; ABK28980, ABK29015.
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                                                                                                                                                                                              1 Similarity 66.7
22; Conservative
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                                                                                                                                                           197 AA;
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                                                           Gaps
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                               Length 197;
                                                         3; Indels
                               23;
                           61.4%; Score 113.5; DB 2 66.7%; Pred. No. 1.6e-07;
                                                      7; Mismatches
                                                                             5 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK 36
                                                                                            AAY66756 standard; protein; 206 AA.
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980S-0088730
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                                      Best_Local Similarity
Matches 22; Conserv
197 AA;
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                                                                                                                                                                                                                                                                                                                           Homo sapiens
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02-JUN-1998;
03-JUN-1998;
04-JUN-1998;
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Sequence
                                                                                                                                                                                                     AAY66756;
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98US-0089598

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The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular, domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor immunoadhesins, for instance, can be used as therapeutic agents. Receptor receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.4%; Score 113.5; DB 21; Length 206; 66.7%; Pred. No. 1.7e-07; ive 7; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Membrane-bound proteins and related nucleotide sequences
                                                                                                                                                                                                                                                                                                                                                      Smith V,
                                                                                                                                                                                                                                                                                                                                                    Baker K, Chen J, Goddard A, Gurney AL, Wood WI, Yuan J;
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                                                               98US-0096960
98US-0097022
                                      98US-0096950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant techniques.
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Best Local Similarity 66.7
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-072883/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 AA;
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                                                               18-AUG-1998;
                                                                                          19-AUG-1998;
20-AUG-1998;
                                                                                                                    24-AUG-1998;
26-AUG-1998;
                                                                                                                                               26-AUG-1998;
26-AUG-1998;
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                                                    .8-AUG-1998
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                                 18-JUN-1998;
18-JUN-1998;
18-JUN-1998;
19-JUN-1998;
19-JUN-1998;
22-JUN-1998;
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24-JUN-1998;
24-JUN-1998;
24-JUN-1998;
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30-JUL-1998;
04-AUG-1998;
04-AUG-1998;
04-AUG-1998;
04-AUG-1998;
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22-JUN-1998
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and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammanian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.

888888888888888

Gaps

Length 206;

Score 113.5; DB 22; Length Pred. No. 1.7e-07; 7; Mismatches 3; Indels

61.4%; 66.7%;

Ouery Match Best Local Similarity 66.7° Matches 22; Conservative

206 AA;

Seguence

36

5 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK

Dp ò

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dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; 
blood; chondrocyte cell; cell proliferation; cell differentiation; colon; 
adrenal; lung; breast; prostate; rectum; cervix; liyer; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Goddard A, Godov
Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Fig 276; 774pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P, Chen J, Desnoyers L, Smith V, Watanabe CK, W
                                                                                                                               03-MAR-2000; 2000US-187202P.
06-MAR-2000; 2000US-186968P.
14-MAR-2000; 2000US-189320P.
14-MAR-2000; 2000US-189328P.
15-MAR-2000; 2000US-190828P.
21-MAR-2000; 2000US-190828P.
21-MAR-2000; 2000US-191007P.
21-MAR-2000; 2000US-191048P.
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2000US-192655P.
2000US-193032P.
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2000WO-US08439.
2000US-194449P.
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2000US-195975P.
                                                                                              28-FEB-2001; 2001WO-US06520
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N-PSDB; AAS46062.
                                                        WO200168848-A2
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21-MAR-2000; 2
28-MAR-2000; 2
29-MAR-2000; 2
30-MAR-2000; 2
30-MAR-2000; 2
                                     Homo sapiens
                                                                                                                                                                                                                                                                                                    11-APR-2000;
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08-NOV-2000;
01-DEC-2000;
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25-APR-2000;
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PJ;
                                                                                                                                                                                                                                                                                                     chromosomal mapping; gene mapping; tissue typing;
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Godowski F
Paoni NF;
                                                                                                                                                                                                                                                                      Human; secreted and transmembrane protein; PRO; cytostatic;
cell death; cancer; chromosomal mapping; gene mapping; tisse
diagnostic assay.
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                                                                                                                                                                                                               Human PRO1345 (UNQ700) protein sequence SEQ ID NO:403.
                                              AAB65279 standard; Protein; 206 AA
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99US-0143048.
99US-0144758.
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2000WO-US04341.
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                                                                                                                                                           02-APR-2001 (first entry)
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Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200073454-A1.
                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ferrara N, Fo
Grimaldi CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-2000;
22-FEB-2000;
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15-SEP-1999;
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                                                                                                          AAB65279;
RESULT 5
                         AAB65279
                                                                                                    ACCOMMENT OF THE PROPERTY OF T
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Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats

Polakis P;

Gurney AL,

Goddard

2000WO-US32678. 2001WO-US06520. 2001WO-US17800.

2001WO-US26626

2001WO-US19692. 2001WO-US21066. 2001WO-US21735.

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(GETH ) GENENTECH INC
                                                                                                                                                                                        Ashkenazi AJ,
               23-AUG-2001;
                                                                                                   20-JUN-2001;
29-JUN-2001;
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                                                                      28-FEB-2001;
                                                                                       01-JUN-2001;
                                          24-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO mucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are
                                                                                                                                                                                                                                                                           used to develop and screen therapeutically useful reagents. The PRO mucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44687 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; tumour-associated antigenic target-173; TAT173; cytostatic; gene therapy; tumour; breast; lung; liver; stomach; cancer; ADEPT; antibody-dependent enzyme mediated prodrug therapy.
                                                                                PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death -
                                                                                                                                                                                                                                                                                                                                                                                                                          Match 61.4%; Score 113.5; DB 22; Length 206; Local Similarity 66.7%; Pred. No. 1.7e-07; les 22; Conservative 7; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human tumour-associated antigenic target-173 (TAT173) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "C-type lectin domain signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126.130
/label= Amidation_site
155.161
/label= N-myristoylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Signal_peptide
12..206
/label= Mature_TAT173_protein
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/label= N·myristoylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : || ||: :|:|| ||: ||:||||||||||| 47 RDKDGDLKTQIEKLWTEVNALKEIQALQTVCLR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170.174
/label= Amidation_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE20465 standard; Protein; 206 AA.
                                                                                                                                            Claim 12; Fig 288; 935pp; English.
Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Stewart TA,
                                         WPI; 2001-032160/04
                                                                                                                                                                                                                                                                                                                                                                                               206 AA;
                                                          N-PSDB; AAF44248.
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Roy MA,
Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; H6FXTN23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                               breast,
                                                                                                                                                                          New antibodies that bind tumor-associated antigenic target (TAT) polypeptides, useful for treating and diagnosing tumor (e.g. breas lung, liver or stomach tumor) in mammals, e.g. dogs, cats, cattle, pigs, goats, rabbits or humans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.4%; Score 113.5; DB 23; Length 206; 66.7%; Pred. No. 1.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 113..., Pred. No. 1.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK 36
A, Godowski PJ,
Wu TD, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW94264 standard; protein; 180 AA.
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                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 10; 124pp; English.
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Matches 22; Conservative
                           Wood WI,
                                                                                   WPI; 2002-292065/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 AA;
                                                                                                                  N-PSDB; AAD32720
                              Williams PM,
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Homo sapiens.

Kastrup JS;

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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family onlypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural moistures to construct comprise at least one tetranectin trimerising structural construct comprise at least one tetranectin trimerising structural moiety, the TYSE being capable of forming a stable complex with 2 other moyof the fusion proteins CIH6FXTN123, H6FXTN124, H6FXTN12, H6FXTN123 (AAW94261 to AAW94261). The TYSE can be used for the construction of structure, a toxin, a detectable label, an in situ activatable substance, an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer, a photo cross-linking agent, or a group facilitating conjugation of the constructs can be used construct to a target. They can be used as vehicles of a sembling antibody fragments into oligomeration multivalent constructs can be used for themedial for transfection or infection of the specific constructs can be used for transfection or infection of the specific constructs can be used for transfection or infection of the specific constructs can be used for transfection or infection of the specific constructs can be used for transfection or infection of the specific constructs can be used for transfection or infection of the specific constructs can be used for transfection or infection of the specific constructs can be used for transfection or threating a substance to a reinmant when a simmading or toxin-conjugated constructs can be used not a naise the navel or transfection or the specific constructs can be used not an also be used for delivering a substance to a reinmant when a simmading the navel or transfer or navention or transfer and the naventing a substance to a reinmant when a simmading the naventing a naventing a publication of the specific constructs.
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                                                                                                                                                                                                                                                                                                                     New monomer polypeptide constructs for diagnosis and therapy - comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
                                                                                                                                                                                      Holtet TL,
                                                                                                                                                                                                                    Thogersen HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 8; 110pp; English.
                                                                                                                                                                                  Graversen NJH,
                                                                  GRAVERSEN N J H.
                                                                                                                                                                                                              Nielsen BB,
                                                                                       HOLTET T L.
KASTRUP J S.
                                                                                                                                                                                                                                                              WPI; 1999-080897/07
                                    ETZERODT M.
                                                                                                                                                                            Etzerodt M,
                                                                                                                                                                                                              Larsen IK,
                                                                                                                                                                                                                                                                                                                                                                                                                   activity
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                                 ETZE/)
                                                                                                                      (KAST/)
                                                                  GRAV/)
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DB 20; 'Length 180; 0.0015; ohes 6; Indels Pred. No. 0.006; Mismatches Score 84; 8 DDLRNEIDKLWREVNSLKEMQALQTVCLK 36 45.48; Conservative Local Similarity tes 17; Conserv Sequence 180 AA; Query Match Matches ò q

Gaps

· .;

23 EELKSRLDTLAQEVALLKEQQALQTVCLK 51

Human tetranectin amino acid sequence. AAW94256 standard; protein; 181 AA. 26-APR-1999 (first entry) AAW94256; AAW94256

Trimeric polypeptide, tetranectin trimerising structural element, TTSE, fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin.

New monomer polypeptide constructs for diagnosis and therapy comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional Kastrup JS; Graversen NJH, Holtet TL Nielsen BB, Thogersen HC; 98WO-DK00245 97DK-0000685 (GRAV/) GRAVERSEN N J H. (HOLT/) HOLTET T L. (KAST/) KASTRUP J S. Nielsen BB, WPI; 1999-080897/07 (ETZE/) ETZERODT M. WO9856906-A1 11-JUN-1998; 11-JUN-1997; Etzerodt M, Larsen IK, activity

Claim 10; Page 60; 110pp; English.

CONSTINCT COMPITIES at least one Lettanettin Limitations of CONSTINCT COMPITIES at least one heterologous molety, the TTSE being capable of forming a stable complex with 2 other molety, the TTSE being capable of forming a stable complex with 2 other any of the fusion proteins CIIH6FYN1013, H6FYN1023, H6FYN1 preselected pharmacokinetic and/or pharmadynamic properties. The constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific population of cells. They can also be used for delivering a substance to antibody to a tumour. They can also be used for prevention or treating a antibody to a tumour. They can also be used for prevention or treating a disease or for diagnosis. The TYSE provides a stable structure which can act as a vehicle for a wide variety of conjugates. The present sequence represents a human tetranectin sequence from which the TYSE can be polypeptide structural elements derived from the tetranectin protéin family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural invention relates to the design of trimeric polypeptides using

Gaps ; 0 45.4%; Score 84; DB 20; Length 181; 58.6%; Pred. No. 0.0016; Live 6; Mismatches 6; Indels 36 8 DDLRNEIDKLWREVNSLKEMQALQTVCLK Conservative Local Similarity 181 AA; 17: Seguence Query Match Matches

52 AA. AAW94262 standard; protein; 197 AAW94262; RESULT 9 AAW94262 Q XXXXXX

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26-APR-1999 (first entry)

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(DENZ-) DENZYME APS
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nes 17; Conserv
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03-DEC-1993;
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                                                                                                            AAR60521;
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                           RESULT 10
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                                                 AAR6052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous moiety, the TTSE being capable of forming a stable complex with 2 other TTSEs, with the proviso that the heterologous moiety is different from any of the fusion proteins CIIHETAN123, HERTAN123, HERTAN12, HERTAN23 (AAW94261 to AAW94261). The TTSE can be used for the construction of conjugates with heterologous moieties such as a ligand binding structure, a toxin, a detectable label, an in situ activatable substance, an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer, a phonomer polypeptide construct to a group facilitating conjugation of the monomer polypeptide construct to a target. They can be used as vehicles for assembling antibody fragments into oligomeric or multivalent configurations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      population of cells. They can also be used for delivering a substance to a cell or tissue or for delivering an imaging or toxin-conjugated antibody to a tumour. They can also be used for prevention or treating a disease or for diagnosis. The TTSE provides a stable structure which can
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                                      Trimeric polypeptide; tetranectin trimerising structural element; TTSE; flusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imagling; tunour; human; tetranectin; H6FXTM123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preselected pharmacokinetic and/or pharmadynamic properties. The constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New monomer polypeptide constructs for diagnosis and therapy comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
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.0017;
6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holtet TL,
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H6FXTN123 fusion protein sequence
                                                                                                                                                                                                                                                                                 98WO-DK00245
                                                                                                                                                                                                                                                                                                                          97DK-0000685
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                                                                                                                                                                                                                                                                                                                                                                                         (GRAV/) GRAVERSEN N J H. (HOLT/) HOLTET T L. (KAST/) KASTRUP J S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nielsen BB,
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les 17; Conser
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cDNA encoding human tetranectin (full sequence given in AAR60521) was PCR amplified using primers given in AAA071274-75. Amplified cDNA was linked to a sequence encoding the Factor-Xa cleavage site (given.in AAR60503), subcloned in vector pT7H6 so that it was linked to a hexahistidine-encoding sequence and expressed in E. coli BL21. The fusion protein was purified on an Ni2+-activated NTR-agarose column. A cyclic procedure was used to obtain correctly folded recombinant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Refolding of polypeptide molecules - using a cyclic process involving denaturing and renaturing conditions to produce a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.4%; Score 84; DB 15; Length 202; 58.6%; Pred. No. 0.0018; iive 6; Mismatches 6; Indels
                                                                                                                                                                                                            Serine protease; Factor-Xa; recognition site; tetranectin; fusion protein cleavage; protein folding; primer; polymerase chain reaction; amplification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thogersen HC;
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AAR60521 standard; Protein; 202 AA.
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93DK-0000139.
93WO-GB02492.
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õ a Kastrup JS;

Holtet TL,

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polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous molety, the TTSE being capable of forming a stable complex with 2 other TTSEs, with the proviso that the heterologous molety is different from any of the fusion proteins CIHERTWIL23. HERTWIL23. H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preselected pharmacokinetic and/or pharmadynamic properties. The constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific population of cells. They can also be used for delivering a substance to a cell or tissue or for delivering an imaging or toxin-conjugated
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                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the design of trimeric polypeptides using
                                                                                                                                                                                                                            New monomer polypeptide constructs for diagnosis and therapy - comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
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Pred. No. 0.0021;
6; Mismatches 6; Indels
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                                                                                                                                     Thogersen HC;
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58.68;
                                                                                                          Graversen NJH,
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GRAV/) GRAVERSEN N J H.
                                                                                                                               Nielsen BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 58.6
Matches 17; Conservative
                           (HOLT/) HOLTET T L.
(KAST/) KASTRUP J S.
                                                                                                                                                                                WPI; 1999-080897/07
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Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trimeric polypeptide: tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; CIIH6FXTN123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            urchin and tomato. These were derived from expressed sequence tags (E from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess blodyversity and for nutritional purposes. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Asundi V;
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0.0018;
ches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                          Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               , Liu C, Zhou P, Qian XB, Wang
Drmanac RA, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.4%; Score 84;
58.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Page 1069; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 DDLRNEIDKLWREVNSLKEMQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIIH6FXTN123 fusion protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW94261 standard; protein; 228
                                                                                                                                                                                                                 2000US-0491404.
2000US-0617746.
2000US-0631451.
                                                                                                                                                           25-JAN-2001; 2001WO-US02687
                                                                                                                                                                                                                                                                                                2000US-0663870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-DK00245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-476164/51.
N-PSDB; AAH98693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 AA;
                                                           WO200154477-A2
          Homo sapiens.
                                                                                                                                                                                                                                                               03-AUG-2000;
15-SEP-2000;
                                                                                                                                                                                                                 25-JAN-2000;
17-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9856906-A1
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                                                                                                            02-AUG-2001
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Query Match

Best Loca Matches

RESULT 12 AAW94261

qq δ

Cao Y,

Gaps

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Kastrup JS;

JH, Holtet TL, Thogersen HC;

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New monomer polypeptide constructs for diagnosis and therapy comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
            Graversen NJH,
                     Nielsen BB,
                                        WPI; 1999-080897/07
                                                                                                                                                                                                                                                                                                                                                                                                                  52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9856906-A1
            Etzerodt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW94270;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                         activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                             Tetranectin is comprised of four polypeptide chains having the formula shown in App60098. Tetranectin stimulates and controls the plasminogen activation resulting in a higher rate of clot lysis or fibrinolysis, esp. in the presence of blood platelets and in the presence of a complex fibrin clot from blood. It stimulates and controls the plasminogen activation in the absence of a cofactor such as polylysine.
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                    New Tetranectin protein - purified from human blood plasma by e.g. affinity chromatography on a column with coupled kringle of plasminogen.
                                                                                                                                                                                                                                                                                                                                             42.7%; Score 79; DB 7; Length 182; 55.2%; Pred. No. 0.0076; tive 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tetranectin polypeptide fragment (residues 1-52).
                                                                                                                                                                                                                                                                                                                                                                                    8 DDLRNEIDKLWREVNSLKEMQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                               24 EELKSRLDTLAQEXALLKEQQALQTVCLK 52
                                                                                                                                                                                                                            Claim 9; Page la; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW94254 standard; Protein; 52
                                                                                                                                              Duhl Clemmensen I, Kluft C;
                                                                                       86EP-0201005
                                                                                                          85NL-0001682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97DK-0000685
                             /label= M,V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                             (NEDE ) NEDERLAND ORG TNO.
77..176
152..168
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GRAV/) GRAVERSEN N J H.
(HOLT/) HOLTET T L.
(KAST/) KASTRUP J S.
                                                                                                                                                                   WPI; 1986-340760/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETZERODT M.
                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 16; Conserv
                                                                                                                                                                                                                                                                                                                           182 AA;
                   Misc-difference 37
 Disulfide-bond
           Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUN-1997;
                                                                                       10-JUN-1986;
                                                                                                          11-JUN-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-DEC-1998
                                                                   30-DEC-1986
                                                EP206400-A.
                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW94254;
                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein (family) The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous moiety, the TTSE being capable of forming a stable complex with 2 other TTSEs, with the proviso that the heterologous moiety is different from any of the fusion proteins CIHEFXTN123, HEFXTN12, HEFXTN12, HEFXTN13 (AAW94261 to AAM94264). The TTSE can be used for the construction of conjugates with heterologous moieties such as a ligand binding structure, a toxin, a detectable label, an in situ activatable substance, an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer, a proup facilitating conjugation of the monomer polypeptide construct to a tranger. They can be used as vehicles for assembling antibody fragments into oligomeric or multivalent configuration of the construction of the construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody to a tumour. They can also be used for prevention or treating a disease or for diagnosis. The TTSE provides a stable structure which can act as a vehicle for a wide variety of conjugates. The present sequence represents a human tetranectin polypeptide fragment. The encoding nucleic acid sequence was amplified by PCR from the plasmid clone pTYH6FXTM133. This is used in the construction of E. coli expression vectors for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preselected pharmacokinetic and/or pharmadynamic properties. The constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific population of cells. They can also be used for delivering a substance to a cell or tissue or for delivering an imaging or toxin-conjugated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
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Pred. No. 0.0082;
6; Mismatches 7; Indels
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Best Local Similarity
Matches 16; Conserv
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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural construct comprise at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous moiety, the TTSE being capable of forming a stable complex with 2 other any of the fusion proteins CIHHERTN123, HERTN123, HERTN124, HERTN123 any of the fusion proteins CIHHERTN123, HERTN123, HERTN124, HERTN123 and conjugates with heterologous moiety as of part activatable substance, and norzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer, and photo cross-linking agent, or a group facilitating conjugation of the monomer polypeptide construct to a target. They can be used as vehicles for generating otherwise into oligomeric or multivalent entitles for generating chimmeric artificial antibodies having preselected pharmacokinetic and/or pharmadynamic properties. The constructs can be used for trangeted gene therapy involving selective delivery of the material for transfection or infection of the specific population of cells. They can also be used for delivering a substance to a rith a title antibody. They can also be used for delivering a substance to a rith a title.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody to a tumour. They can also be used for prevention or treating a disease or for diagnosis. The TTSE provides a stable structure which can act as a vehicle for a wide variety of conjugates. The present sequence represents a H6FXtripa fusion protein sequence encoded by the plasmid
                                                                                                                                                                                                                                                                                                                                                      New monomer polypeptide constructs for diagnosis and therapy - comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
                                                                                                                                                                                                                                              , Graversen NJH, Holtet TL, Kastrup JS;
Nielsen BB, Thogersen HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 4; 110pp; English.
                                              98WO-DK00245
                                                                                     97DK-0000685
                                                                                                                                                   (GRAV') GRAVERSEN N J H.
(HOLT/) HOLTET T L.
(KAST/) KASTRUP J S.
                                                                                                                                                                                                                                                                                                          WPI; 1999-080897/07
                                                                                                                                   ETZERODT M.
                                           11-JUN-1998;
                                                                                     11-JUN-1997;
17-DEC-1998.
                                                                                                                                                                                                                                           Etzerodt M,
                                                                                                                                                                                                                                                              Larsen IK,
                                                                                                                            (ETZE/) | (GRAV/) (HOLT/) |
                                                                                                                                                                                                                                                                                                                                                                                                                         activity
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73 AA; Sequence

. 0 Query Match
40.0%; Score 74; DB 20; Length 73;
Best Local Similarity 55.2%; Pred. No. 0.012;
Matches 16; Conservative 6; Mismatches 7; Indels

Gaps

Ωp ð

Search completed: April 15, 2003, 11:48:00 Job time : 29.75 secs

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US-08-486-56

Sequence 56, Application US/08469486

Patent No. 5739381

GENERAL INFORMATION:
APPLICANT: Thoegersen, Hans Christian
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of TITLE OF INVENTION: proteins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                           Sequence 99, Application US/09602877A Patent No. 6432707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.4%;
ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapien
US-09-602-877A-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boston
                                                                                                                                                                                                                                                                       RESULT 1
US-09-602-877A-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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Sequence 14, Appl
Sequence 29, Appl
Sequence 3704, Ap
Sequence 6, Appli
Sequence 7, Appli
Sequence 8, Appli
Sequence 1, Appli
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                                                                    April 15, 2003, 11:45:59 ; Search time 10 Seconds (without alignments) 105.923 Million cell updates/sec
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being printed,
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Sequence 32, Alg
Sequence 2, App
Sequence 176, A
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Sequence 6, ₽
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Sequence 12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2
Sequence 4
Sequence 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Sequence 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to h score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                   262574
                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
version 5.1.4_p5_4578 - 2003 Compugen Ltd.
                                                                                                                                               36
                                                                                                                                   185
1 SKSGKGKDDLRNEIDKLWREVNSLKEMQALQTVCLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-602-877A-99
US-08-469-486-56
US-08-469-658-66
US-08-178-477B-32
US-09-314-112-2
US-09-513-783A-176
US-09-685-199B-2
US-09-085-199B-4
US-09-085-199B-5
US-09-085-199B-5
US-09-452-199B-5
US-08-45-199B-1
US-08-45-199B-1
US-08-487-826B-1
US-08-487-826B-1
US-08-487-826B-14
US-08-178-477B-29
US-08-178-477B-29
US-08-178-477B-29
US-08-178-477B-29
US-08-178-477B-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -956-307B-17
                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -08-178-477B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-470-512A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·08-956-307B-1
                                                                                                                                                                                                         262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
 GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                              Issued_Patents_AA:*
                                                                                                                                                                                                                                                         seq length: 0
seq length: 200000000
                                                                                                                       US-09-445-576A-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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2710
3060
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                      Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.5
55.5
55.5
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Maximum DB
                                                OM protein
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                                                                       Run on:
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8
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4187, Ap
4, Appli
4, Appli
                  18, Appl
7, Appli
3627, Ap
10, Appl
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2, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                               Length. 197;
                                                                                                                                                                                                                                                  GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER

FILE REFERENCE: 210121.44655

CURRENT APPLICATION NUMBER: US/09/602,877A

CURRENT FILING DATE: 2000-06-22

NUMBER: PSEQ ID NOS: 107

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 99
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                         US-08-452-592B-7
US-09-134-001C-3627
US-07-91-867B-10
US-08-107-755A-10
US-09-370-861A-10
US-09-134-001C-4187
US-09-134-001C-4187
US-09-134-001C-5178
US-09-134-001C-5178
US-09-134-001C-5178
                                                                                                                                                                                                                                                                                                                                                                                                             Score 113.5; DB 4
Pred. No. 4.5e-08;
7; Mismatches 3
                                                                                                                                                         US-08-469-537A-103
                                                                                                                             -08-442-248-2
-08-440-815-2
-08-486-449-2
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42
76
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Application US/08178477B
Patent No. 5756343
GENERAL INFORMATION:
APPLICANT: WESTWOOD, J. TIMOTHY.; RABINDRAN, SRIDHAR
TITLE OF INVENTION: CELL STRESS
TITLE OF SEQUENCES: 42
                                                                                                                                                                                                                                                                    45.4%; Score 84; DB 2; 158.6%; Pred. No. 0.00047; tive 6; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 57; DB 1;
Pred. No. 6.5;
7; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/178,477B
FILING DATE: 07-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                      8 DDLRNEIDKLWREVNSLKEMQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/617,910
FILING DATE: 26-NOV-1990
CLASSIFICATION: 530
            TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 2026
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEX: 421792
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: MORGAN & FINNEGAN
345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 30.8%;
Best Local Similarity 37.1%;
Matches 13; Conservative
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 58.69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-469-658-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-178-4778-32
                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: NEW YORK
                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
STREET: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-178-477B-32
                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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Patent No. 5917018
GENERAL INFORMATION:
APPLICANT: Th egersen, Hans Christian
APPLICANT: Ezerodt, Michael
TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
45.4%; Score 84; DB 1; 1
Best Local Similarity 58.6%; Pred. No. 0.00047;
Matches 17; Conservative 6; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIF: 0110-2804

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FLING DATE: June 5, 1995
CLASSIFICATION: 530
                                                                                                                      FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 0653/002001
TELEPHONE: 617 542 8906
TELEFAX: 617 542 8906
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acids
TELES: amino acids
TELES: amino acids
TELES: amino acids
                                          Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 DDLRNEIDKLWREVNSLKEMQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 EELKSRLDTLAQEVALLKEQQALQTVCLK 73
                                                        SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486
                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
CLASSIFICATION: 530
      IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-486-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Massachusetts
COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
STATE: Massac
                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-469-658-56
                                        SOFTWARE
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COMPUTER:
                                                         STREET: CITY: Ber STATE: M. COUNTRY:
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US-09-085-199B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-951-871-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: VOELIMY, Richard
TITLE OF INVENTION: MOLECULAR REGULATORY CIRCUITS TO ACHIEVE
TITLE OF INVENTION: SUGTAINED ACTIVATION OF GENES OF INTEREST BY A SINGLE STRESS
FILE REFERENCE: 870109.409
CURRENT PELING DAMER: US/09/304,121
CURRENT FILING DAME: 3
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FASTSEQ for Windows Version 3.0
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FENTION: METHOD FOR CLONING
FENTION: AND PRODUCING THE BS11 RESTRICTION ENDONUCLEASE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: GFP-HSF1
US-09-513-783A-176
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Giuliano, Kenneth A.
APPLICANT: Kapur, Ravi
TITLE OF INVENTION: A System for Cell Based Screening
FILE REFERENCE: 97-022-L1
CURRENT APPLICATION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 57; DB 4;
Pred. No. 10;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                   402 KGKQECMDSKLLAMKHENEALWREVASLRQKHAQQ 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.8%; Score 57; DB 37.1%; Pred. No. 6.5; tive 7; Mismatches
--- LRNEIDKLWREVNSLKEMQALO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 KGKDD-----LRNEIDKLWREVNSLKEMQALQ 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 176, Application US/09513783A Patent No. 6416959 GENERAL INFORMATION:
                                                                                                                               Sequence 2, Application US/09304121 Patent No. 6342596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08951871
Patent No. 5866398
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 30.8%;
Best Local Similarity 37.1%;
Matches 13; Conservative
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APPLICANT: XIAO, JIAN-PING
TITLE OF INVENTION: METHOD
TITLE OF INVENTION: AND PRG
TITLE OF INVENTION: COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 30.8
Best Local Similarity 37.1
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapien
US-09-304-121-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-513-783A-176
5 KGKDD---
                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2
                                                                                           RESULT 5
US-09-304-121-2
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LENGTH: 783
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 57; DB 2; Length 912; Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette, 3.50 inch, 1.44 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
             ADDRESSEE: New England Biolabs, Inc. STREET: 32 Tozer Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 KDDLRNEIDKLWREVNSLKEMQALQTVCL 35
                                                                                                                                                                       SOFTWARE: FASTEM: DOS
SOFTWARE: FASTSEQ VETSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,871
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Huq, A.H.M. Mahbubul
APPLICANT: Chopra, Vikramjit Singh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/09085199B
; Patent No. 6235879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MS DOS 5.0
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STREET: PO Box 5270
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                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION
TELEPHONE: 978-927-5054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.8%;
                                                                                                                                                   E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 912 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                              NAME: Williams, Gregory REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM Compatibl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 37.9
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 978-927-1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WordPerfect
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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CORRESPONDENCE ADDRESS:
                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COM
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Hayden.
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CITY: Frisco
STATE: CO.
                                                   Beverly
                                                                                                                                               MEDIUM TYPE:
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APPLICANT: Hug, A.H.M. Mahbubul
APPLICANT: Chopra, Vikramjit Singh
APPLICANT: Kalchman, Michael
TITLE OF INVENTION: Apoptosis Modulators That Interact with the
                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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                                                                                                                                                                                                                                                                                             Indels
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MEDIUM TYPE: Diskette, 3.50 inch, 1.44 kb storage COMPUTER: IBM Compatible OPERATING SYSTEM: MS DOS 5.0 SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Huntington-interacting protein
                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
                                                                                                                                                                                                                    Query Match 30.0%; Score 55.5; D
Best Local Similarity 33.3%; Pred. No. 19;
Matches 11; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         30.0%; Score 55.5; C
33.3%; Pred. No. 24;
tive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                        1 SKSGKGKDDLRNEIDKLWREVNSLK-EMQALQT 32
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Huntington-interacting protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Larson, Marina T.
REGISTRATION NUMBER: 32038
REFERENCE/DOCKET NUMBER: UBC.P-013US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 5, Application US/09085199B ; Patent No. 6235879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Oppedahl & Larson
PO Box 5270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hayden. Michael R.
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TELEFAX: (970) 668-2052
INFORMATION FOR SEQ ID NO: 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 33.33
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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HYPOTHETICAL: no ...
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
3Y: linear
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ZIP: 80443-5270
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                                                HYPOTHETICAL: DORIGINAL SOURCE: ORGANISM: hum
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CITY: Frisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                               ; FEATURE: HIUS-09-085-199B-4
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APPLICANT:
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APPLICANT: Hackam, Abigail
APPLICANT: Hackam, Abigail
APPLICANT: Constant of the constant of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 386;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Huntington-interacting protein US-09-085-1998-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIE: 80443-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 30.0%; Score 55.5; Di
Best Local Similarity 33.3%; Pred. No. 7.2;
Matches 11; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SKSGKGKDDLRNEIDKLWREVNSLK-EMQALQT 32
                                                                                                             NAME: Larson, Marina T.
REGISTRATION NUMBER: 32038
REGISTRATION NUMBER: UBC.P-013US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2052
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/09/085,199B
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/085,199B
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CORRESPONDENCES: 4
ADDRESSEE: Oppedahl & Larson
STREET: PO BOX 5270
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REGISTRATION NUMBER: 32038
REFERENCE/DOCKET NUMBER: UF
                           FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO. 4: SEQUENCE CHARACTERISTICS: LENGTH: 914
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                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: no
ORIGINAL SOURCE:
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                               amino acid
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TOPOLOGY: linear
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APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellow, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 84;
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                       Diskette, 3.50 inch, 2.0 MB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,459A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Knobbe Martens Olson & Bear
O Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                              MEDIUM 11FE.

COMPUTER: DATA CONTROLL

CONTROLL

SOFTWARE: WordPerfect Version 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/452,592B

FILING DATE: 25 May 1995

CLASSIFICATION DATA:

APPLICATION NUMBER: 08/068,948

FILING DATE: 25 May 1993

ATTORNEY/AGENT INFORMATION:

NAME: Lamming, JOhn H.

NAME: Lamming, JOhn H.

NAME: Ranucci, Vincent J.

REGISTRATION NUMBER: 22,062 (Donahue REGISTRATION NUMBER: 29,579 (Lamming REGISTRATION NUMBER: 29,579 (Ranucci TELECOMMUNICATION INFORMATION:

REFERENCE/DOCKET NUMBER: 34,857 (Lamming REGISTRATION NUMBER: 29,579 (Ranucci TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

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TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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CITY: Newport Beach
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08568459A Patent No. 5849306
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 DLRNEIDKLWREVNSLKEMOA 29
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Chitnis, Chetan
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45 DLKNKVAQLEREVRSLKDKAA
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Best Local Similarity 52.4
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 amino acids
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Mari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
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US-08-568-459A-12
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APPLICANT:
APPLICANT:
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                                                                         GENERAL INFORMATION:
APPLICANT: McGrath, Kevin P.
APPLICANT: Kaplan, David L.
TITLE OF INVENTION: Fabrication of Nanoscale Materials Using TITLE OF INVENTION: Fabrication of Nanoscale Materials Using TITLE OF INVENTION: Self-Assembling Proteins NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. Army Soldier Systems Command STREET: ...i.c.i.c.c.c. (Patent Counsel)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nanoscale Materials Using
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e; Indels
                                                                                                                                                                                                                                                                     STREET:
CITY: Natick
STATE: Massachsuetts
STATE: Massachsuetts
COUNTRY: United States of America
2.PP: 01760-503
COMPUTER: ED50-504
COMPUTER: Diskette, 3.50 inch, 2.0 MB storage
COMPUTER: IBM PC Compatable
OPERATING SYSTEM: DOS 6.22
SOFTWARE: WordPerfect Version 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,592B
FILING DATE: 25 May 1995
''TASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: U.S. Army Soldier Systems Command
AMSCC-CC (Patent Counsel)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: McGrath, Kevin P.
APPLICANT: McGrath, Land L.
APPLICANT: McGrath, David L.
TITLE OF INVENTION: Fabrication of Nanoscale
TITLE OF INVENTION: Self-Assembling Proteins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. AIMY SOLdier Systems Comman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 22,062 (Donal REGISTRATION NUMBER: 34,857 (Lamm. REGISTRATION NUMBER: 29,579 (Ranuc REFERENCE/DOCKET NUMBER: NA-1096D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/068,948
FILING DATE: 25 May 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08452592B Patent No. 5712366
                                   Sequence 9, Application US/08452592B
Patent No. 5712366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FELECOMMUNICATION INFORMATION TELEPHONE: 508-233-4510
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45 DLENEVAQLEREVRSLKDKAA 65
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Lamming, John H.
Ranucci, Vincent J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Massachsuetts
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Matches 12; Conserva
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              08-452-592B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-452-592B-9
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US-08-452-592B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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STATE:
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Best Local Similarity
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ORGANISM: Pla
US-09-210-288-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                        US-09-210-288-12
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ENTHROCYTE BINDING PROTEINS
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                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                      Length 2710;
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Pred. No. 1.5e+02;
4; Mismatches 7; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: Knobbe Martens Olson & Bear
1: 620 Newport Center Drive 16th Floor
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/08487826B Patent No. 5993827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum
                                                                                                                                                                                                                                                                                                      547 KSGKGHDDIEEKLNKFCDEKN 567
                      TELEPANE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2710 amino acids
                                                                                                                                                                                                                                                                                   2 KSGKGKDDLRNEIDKLWREVN 22
                                                                                                                                                                                                                                28.68;
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Matches 10; Conservative
                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                   single
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                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                     ORIGINAL SOURCE:
CREANISM: Pla
US-08-568-459A-12
                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM:
US-08-487-826B-12
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                                                                                                                                                                                                                             Query Match
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APPLICANT: Sim, Kim L.
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Wellems, Thomas E.
APPLICANT: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: BINDING PRASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                 Length 2710;
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Ouery Match 28.6%; Score 53; DB 2; Length 271
Best Local Similarity 47.6%; Pred. No. 1.5e+02;
Matches 10; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: April 15, 2003, 11:51:52 Job time: 12 secs
                                                                                                                                                                                                                                                                Sequence 12, Application US/09210288
Patent No. 6392026
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                                                                                                                             547 KSGKGHDDIEEKLNKFCDEKN 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                               2 KSGKGKDDLRNEIDKLWREVN 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: FULLEr, Michael
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NII
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     547 KSGKGHDDIEEKLNKFCDEKN 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KSGKGKDDLRNEIDKLWREVN 22
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MOLECULE TYPE: protein
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Sequence 403, Sequence 403, Sequence 403,

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Sequence 403 Sequence 276

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Length 36;
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2.8e-18;
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Patent No. US20020156007A1

GENERAL INFORMATION:
APPLICANT: GRAVERSEN, JONAS
APPLICANT: GRAVERSEN, JONAS
APPLICANT: MOESTRUP, SOLEN
FILLE OF INVENTION: APOLITPOPROTEINS ANALOGUES
FILE OF INVENTION: APOLITPOPROTEINS ANALOGUES
FILE OF INVENTION: APOLITPOPROTEINS ANALOGUES
FILE OF INVENTION: APOLITOP OF THE COURSENT OF SOLE APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2001 00657
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEO ID NOS: 91
SEQ ID NO 42
LENGTH: 36
                                                      US-10-175-752-276
US-10-176-48-276
US-10-176-913-276
US-10-176-913-276
US-10-180-552-276
US-10-180-552-276
US-09-990-562-403
US-09-997-428-403
US-09-997-428-403
US-09-997-428-403
US-10-173-700-276
US-10-174-572-276
US-10-174-579-276
US-10-174-578-276
US-10-174-578-276
US-10-174-578-276
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US-10-175-743-276
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Patent No. US20020156007A1
GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
APPLICANT: MOESTRUP, SOTEN
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Carcharhinus springeri
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US-09-987-107-41
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   TYPE: PRT
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403, App
276, App
276, App
276, App
403, App
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                                                                                                                                                                                                                                                        (without alignments)
220.090 Million cell updates/sec
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403,
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/cgn2_6/ptodate/2/pubpaa/PCT_NEW_PUB.pep:*
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                              GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd:
                                                                                                                                                                                                                                                                                                                                                                                                                        SKSGKGKDDLRNEIDKLWREVNSLKEMQALQTVCLK 36
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US-09-992-598-403
US-09-999-735-403
US-09-999-745-403
US-09-990-444-403
US-09-990-436-403
US-09-990-436-403
US-09-991-181-403
US-09-993-687-403
US-09-993-687-403
US-09-993-687-403
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US-09-997-555-2
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US-10-175-737-276
US-09-993-667-403
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US-09-987-107-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248812 seqs, 61136040 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Query
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Perfect score:
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Gaps

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Indels

Result Š. us-09-445-576a-39.rapb

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DB 9; Length 206;
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Pred. No. 8.1e-08;
7; Mismatches 3
              CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: 60/081,071
PRIOR APPLICATION NUMBER: 60/085,697
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-08-15
PRIOR FILING DATE: 1998-08-16
PRIOR FILING DATE: 1998-09-24
PRIOR PELICATION NUMBER: 60/101,922
PRIOR PELICATION NUMBER: 60/101,922
PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1998-09-24
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-03-08
PRIOR FILING DATE: 1999-06-01
PRIOR PELICATION NUMBER: PCT/US99/0508
PRIOR FILING DATE: 1999-06-01
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PRIOR FILING DATE: 2000-03-28
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PRIOR PPLICATION NUMBER: PCT/US01/13692
PRIOR PLING DATE: 2001-06-20
PRIOR PPLICATION NUMBER: PCT/US01/13692
PRIOR PLING DATE: 2001-06-20
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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
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Best Local Similarity 66.7
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-938-418-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICANT: Reed, Steven G.
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.446D1
CURRENT APPLICATION NUMBER: US/09/745,288
CURRENT APPLICATION NUMBER: US/09/745,288
NUMBER OF SEQ ID NOS: 101
SSCTUMBER: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 197;
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3;
       CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR PILING DATE: 2000-01-15
PRIOR PILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin version 3.1
LENGTH: 36
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Pred. No. 3.56
6; Mismatches
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61.4%; Score 113.5;
Best Local Similarity 66.7%; Pred. No. 7.7e
Matches 22; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK 36
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Patent No. US20010018058A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/09938418
Patent No. US20020161199A1
GENERAL INFORMATION:
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1 Similarity 72.7%;
24; Conservative (
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Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polakis, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Wu, Thomas D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CORGANISM: Homo sapien
US-09-745-288-99
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                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Box taurus
US-09-987-107-41
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Matches 2
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Gerber, Hanspeter

APPLICANT:

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APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090445
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/089599
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/090246
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FILING DATE: 1998-06-22
 60/088655
                                                                 APPLICATION NUMBER: 60/088738
                                                                                                  APPLICATION NUMBER: 60/088742
                                                                                                                                 APPLICATION NUMBER: 60/088810
                                                                                                                                               FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088824
                                                                                                                                                                                                 APPLICATION NUMBER: 60/088826
                                                                                                                                                                                                                                  PLICATION NUMBER: 60/088858
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/088876 FILING DATE: 1998-06-11
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/089105
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                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/089512
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FILING DATE: 1998-06-16
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FILING DATE: 1998-06-18
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
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                                PLICATION NUMBER: 60/088734
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CURRENT APPLICATION NUMBER: US/09/992,598
PRIOR APPLING DATE: 2001-11-14
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R APPLICATION NUMBER: 60/065186

R FILING DATE: 1997-11-12

R FILING DATE: 1997-11-13

R FILING DATE: 1997-11-13

R PELING DATE: 1997-11-24

R FILING DATE: 1997-11-24

R APPLICATION NUMBER: 60/06570

R APPLICATION NUMBER: 60/06570
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APPLICATION NUMBER: 60/078910
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088028
FILING DATE: 1998-06-04
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TELING DATE: 1998-05-20
TITING DATE: 1998-06-02
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APPLICATION NUMBER: 60/062250
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APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/088030
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-03
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LING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088217
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                                                  Grimald1, J. Christopher
                                                                                                                                                                                Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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Stewart, Timothy
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                                                                                                                              Paoni, Nicholas F
 Gerritsen, Mary E
                                                                 Gurney, Austin L.
                                                                                   Kljavin, Ivar J
                                                                                                  Napier, Mary A.
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                                                                                                                  an, James
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APPLICANY: Zhang, Zemin
TITLE OF INVENTION. Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION. Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION. Acids Encoding the Same
CURRENT FILING DATE: 1297-00-16
FRIGH RELIGATION NUMBER: 02/09/989,293A
FROM PRICAMING DATE: 1297-00-16
FROM PRICAMING DATE: 1297-00-16
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR APPLICATION NUMBER: 60/08855
PRIOR PELING DATE: 1998-06-09
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088742
                                                                                                                                                                        Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
                                                                                                           Roy, Margaret Ann
Stewart, Timothy
                                                                          aoni, Nicholas F
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Best Local Similarity 66.7%; Pred. No. 8.1e-08;
Matches 22; Conservative 7; Mismatches 3
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PRIOR APPLICATION NUMBER: 60/090535
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PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090863
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091478
PRIOR PELING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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Gurney,Austin L.
Kljavin,Ivar J.
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Gerber, Hanspeter
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Botstein, David
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Eaton, Dan L.
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US-09-989-293A-403
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R FILING DATE: 1998-06-10
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R APPLICATION NUMBER: 60/088826
R APPLICATION NUMBER: 60/088886
R APPLICATION NUMBER: 60/0888888
R FILING DATE: 1998-06-11
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R APPLICATION NUMBER: 60/089952
R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/090246
R FILING DATE: 1998-06-22
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LING DATE: 1998-06-16
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090429
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APPLICATION NUMBER: 60/090431
FILING DATE: 1998-06-24
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FILLING DATE: 1998-06-24
APPLICATION NUMBER: 60/09044
APPLICATION NUMBER: 60/090445
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APPLICATION NUMBER: 60/089105
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APPLICATION NUMBER: 60/089532
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ILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089908
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/089801
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Gaps Length 206; Indels .1e-08 DB Score 113.5; E Pred. No. 8.1e-7; Mismatches 5 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK 36 47 RDKDGDLKTQIEKLWTEVNALKEIQALQTVCLR 79 R APPLICATION NUMBER: 60/091360
R FILING DATE: 1998-07-01
RR APPLICATION NUMBER: 60/091478
RR FILING DATE: 1998-07-02
RR APPLICATION NUMBER: 60/091544
RR FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 APPLICATION NUMBER: 60/090694 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090695 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/090863 APPLICATION NUMBER: 60/091626 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091633 FILING DATE: 1998-07-02 LICATION NUMBER: 60/090676 APPLICATION NUMBER: 60/090678 APPLICATION NUMBER: 60/090696 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/091519 APPLICATION NUMBER: 60/091978 APPLICATION NUMBER: 60/090690 Query Match 61.4%; Best Local Similarity 66.7%; Matches 22; Conservative FILING DATE: 1998-06-26 FILING DATE: 1998-06-25 1998-06-25 FILING DATE: 1998-06-25 FILING DATE: 1998-07-02 FILING DATE: 1998-07-07 FILING DATE: 1998-06-25 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR qq

US-09-989-735-403
. Sequence 403. Application US/09989735
. Publication No. US20020193299A1
. GENERAL INFORMATION: Grimaldi, J. Christopher Roy, Margaret Ann Stewart, Timothy A Ferrara, Napoleone Gerritsen, Mary E. Goddard, Audrey Paoni, Nicholas F. Gerber, Hanspeter Gurney, Austin L. APPLICANT: Ashkenazi, Avi J. Kljavin, Ivar J Napier, Mary A. Botstein, David Baker, Kevin P. Desnoyers, Luc Godowski, Paul Fong, Sherman Eaton, Dan APPLICANT: APPLICANT: APPLICANT

Tumas, Daniel Watanabe, Colin K. Williams, P. Mickey

APPLICANT:

60/088876 APPLICATION NUMBER: 60/089105 NUMBER: 60/089440 1998-06-16 NUMBER: 60/089512 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089538 ICATION NUMBER: 60/089532 APPLICATION NUMBER: 60/089599 60/089653 APPLICATION NUMBER: 60/089801 806680/09 APPLICATION NUMBER: 60/089948 PPLICATION NUMBER: 60/089952 APPLICATION NUMBER: 60/090246 APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/089947 PPLICATION NUMBER: 60/090254 60/090349 APPLICATION NUMBER: 60/090355 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090435 APPLICATION NUMBER: 60/090535 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090431 APPLICATION NUMBER: 60/090444 ILLING DATE: 1998-06-24 60/090445 APPLICATION NUMBER: 60/090540 APPLICATION NUMBER: 60/090472 PRIOR APPLICATION NUMBER: 60/090542 APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090676 1998-06-16 1998-06-18 1998-06-18 1998-06-17 998-06-18 1998-06-1 1998-06-17 998-06-19 998-06-19 998-06-19 1998-06-22 1-90-866 .998-06-23 1998-06-1 998-06-22 1998-06-24 1998-06-1 998-06-23 .998-06-998-06-24 998-06-24 -90-8661 1998-06-ILING DATE: 1998-06-2 998-06-2 998-06-2 -90-866 PLICATION NUMBER: LING DATE: 1998-06 -90-866 FILING DATE: 1998-06 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: PLICATION NUMBER: FILING DATE: 1998-06 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-06 CATION NUMBER: ILING DATE: 1 ILING DATE: 1 FILING DATE: FILING DATE: NG DATE: 'ILING DATE: ILING DATE: LING DATE: FILING DATE: PRIOR PRIOR
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PRIOR PRIOR PRIOR PPLICANT: Zhang, Zemin ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/989,735 CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12 FILING DATE: 1997-11-12 APPLICATION NUMBER: 60/065311 FILING DATE: 1997-11-13 APPLICATION NUMBER: 60/078910 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/083322 FILING DATE: 1997-11-13 APPLICATION NUMBER: 60/066770 APPLICATION NUMBER: 60/075945 FILING DATE: 1998-02-25 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/084600 PPLICATION NUMBER: 60/087609 ILING DATE: 1998-06-02 LICATION NUMBER: 60/087106 LICATION NUMBER: 60/087759 ING DATE: 1998-06-02 PPLICATION NUMBER: 60/088026 ILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088030 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088033 PPLICATION NUMBER: 60/087607 PLICATION NUMBER: 60/088025 LING DATE: 1998-06-04 PELICATION NUMBER: 60/088028 ILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088029 FILING DATE: 1998-06-04 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088326 PRIOR FILING DATE: 1998-00-00
PRIOR APPLICATION NUMBER: 60/088217 60/087827 LICATION NUMBER: 60/088021 60/088202 APPLICATION NUMBER: 60/088167 APPLICATION NUMBER: 60/088212 APPLICATION NUMBER: 60/088655 APPLICATION NUMBER: 60/088738 APPLICATION NUMBER: 60/088742 60/088734 60/088826 998-05-07 998-06-02 998-05-28 998-06-03 1998-06-04 998-06-05 1998-06-05 1998-06-04 60-90-866 998-06-10 998-06-10 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-10 998-06-1 REFERENCE: P2730P1C61 LICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: ILING DATE: LING DATE: LING DATE: FILING DATE: FILING DATE: FILING DATE: LING DATE: LING DATE: FILING DATE: FILING DATE: LING LING PRIOR
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/087106
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PRIOR APPLICATION NUMBER: 60/089105
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Pred. No. 8.1
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR PILING DATE: 1998-06-25
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PRIOR APPLICATION NUMBER: 60/090863
PRIOR APPLICATION NUMBER: 60/091860
PRIOR PILING DATE: 1998-06-26
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PRIOR PELING DATE: 1998-07-01
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PRIOR APPLICATION NUMBER: 60/09154
PRIOR APPLICATION NUMBER: 60/09154
PRIOR PELING DATE: 1998-07-02
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Williams, P. Mickey
Wood, William I.
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66.7%;
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Stewart, Timothy A
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Gerritsen,Mary E
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Best Local Similarity 66.7
Matches 22; Conservative
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Botstein, David
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APPLICATION NUMBER: 60/089532
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PPLICATION NUMBER: 60/090246
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PPLICATION NUMBER: 60/089908
PPLICATE: 1998-06-18
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FILING DATE: 1998-06-17
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ILING DATE: 1998-06-22
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ING DATE: 1998-06-23
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ILING DATE: 1998-06-24
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ILING DATE: 1998-06-24
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ILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090676
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC69
CURRENT APPLICATION NUMBER: US/09/989,730
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Sequence 403, Application US/09989730
Publication No. US20020197674A1
GENERAL INFORMATION:
                                                                             APPLICATION NUMBER: 60/091544
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
                                     APPLICATION NUMBER: 60/091478
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FILING DATE: 1998-07-09
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILLING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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Williams, P. Mickey
Wood, William I.
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Fong, Sherman
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Stewart, Timothy
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Best Local Similarity 66.73
Matches 22; Conservative
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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Eaton, Dan L.
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1997-11-13 1997-11-24 1997-11-24 1998-02-25 1998-02-20 1098-03-20 1098-03-20 1098-04-28 1098-04-28 1098-04-28 1098-05-07 1098-05-07 1098-05-28 1098-05-28 1098-05-28	FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/APPLICATION NUMBER: 60/2 APPLICATION NUMBER: 60/APPLICATION NUMBER: 60/FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/APPLICATION DATE: 1998-06-04	APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04 PPLLICATION NUMBER: 60/ FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-09 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-09 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-09	60/0887 6-10 6-10 6-10 6-10 6-10 60/0888 6-10 60/0888 6-10 60/0888 6-10 60/0888 6-10 60/0888 6-10 60/0888 6-10 60/0895

PRIOR APPLICATION NUMBER: 60/08953 PRIOR APPLICATION NUMBER: 60/08959 PRIOR FILING DATE: 1998-06-17 PRIOR PILING DATE: 1998-06-17 PRIOR PILING DATE: 1998-06-17 PRIOR FILING DATE: 1998-06-17 PRIOR FILING DATE: 1998-06-17 PRIOR FILING DATE: 1998-06-18 PRIOR PILING DATE: 1998-06-19 PRIOR FILING DATE: 1998-06-19 PRIOR FILING DATE: 1998-06-22 PRIOR FILING DATE: 1998-06-22 PRIOR FILING DATE: 1998-06-22 PRIOR PILING DATE: 1998-06-22 PRIOR PILING DATE: 1998-06-24 PRIOR PILING DATE: 1998-06-25 PRIOR PILING DATE: 1998-06

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APPLICATION NUMBER: 60/084600
FILLING DATE: 1998-05-07
APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/088033
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ING DATE: 1998-06-05
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APPLICATION NUMBER: 60/088734
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/089440
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ILING DATE: 1998-06-10
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FILING DATE: 1998-06-11
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PRIOR APPLICATION NUMBER: 60/089514
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PRIOR APPLICATION NUMBER: 60/089532
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APPLICATION UNMBER: 60/089598
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089599
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APPLICATION NUMBER:
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CURRENT APPLICATION NUMBER: US/09/990,436
PRIOR APPLICATION NUMBER: 60/049787
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Best Local Similarity 66.7%; Pred. No. 8.1e-08;
Matches 22; Conservative 7; Mismatches 3
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US-09-990-436-403
Sequence 403, Application US/09990436
Publication No. US20020198148A1
GENERAL INFORMATION:
APPLICANT: AshRemazi, Avi J.
APPLICANT: Baker Kevin P.
APPLICANT: Beck Kevin P.
APPLICANT: Box E. Luc
                                                                                      FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091626
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091633
                           60/091544
                                                                  APPLICATION NUMBER: 60/091519
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APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
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FILING DATE: 1998-07-07
PPLICATION NUMBER: 60/092182
FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/062250
FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/065186
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APPLICATION NUMBER: 60/065311
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APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
            LICATION NUMBER: 60/
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Stewart, Timothy A.
Tumas, Daniel
FILING DATE: 1998-07-02
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Gerber, Hanspeter
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                                             FILING DATE:
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FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090678
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090690
APPLICATION NUMBER: 60/089600
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089653
                                            FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089801
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089907
FILING DATE: 1998-06-18
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948
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APPLICATION NUMBER: 60/090246
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APPLICATION NUMBER: 60/090349
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PLICATION NUMBER: 60/090435
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PLICATION NUMBER: 60/090472
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PLICATION NUMBER: 60/090542
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APPLICATION NUMBER: 60/090694
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090695
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APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091626
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APPLICATION NUMBER: 60/089908
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APPLICATION NUMBER: 60/090252
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APPLICATION NUMBER: 60/090254
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PLICATION NUMBER: 60/090431
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-26
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                                           61.4%; Score 113.5; DB 9 66.7%; Pred. No. 8.1e-08; Live 7; Mismatches 3
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CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
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US-09-991-181-403
September 403, Application US/09991181
Publication No. US20020197615A1
GENERAL INFORMATION:
                                 PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
60/091633
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APPLICATION NUMBER: 60/062250
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APPLICATION NUMBER: 60/065186
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APPLICATION NUMBER: 60/066770
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APPLICATION NUMBER: 60/075945
FILING DATE: 1998-02-25
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APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/065311
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APPLICATION NUMBER: 60/087607
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Grimaldi, J.Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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APPLICANT: Baker,Kevin P.
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APPLICATION NUMBER:
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Best Local Similarity
Matches 22; Conserv
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R APPLICATION NUMBER: 60/091360
R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091478
R FILING DATE: 1998-07-02
R APPLICATION NUMBER: 60/091544
R FILING DATE: 1998-07-01 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089947 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089948 APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090246 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 60/090252 60/090349 60/090355 APPLICATION NUMBER: 60/090254 APPLICATION NUMBER: 60/090429 APPLICATION NUMBER: 60/090445 60/090472 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090676 60/090431 APPLICATION NUMBER: 60/090535 APPLICATION NUMBER: 60/090540 APPLICATION NUMBER: 60/090542 60/090557 APPLICATION NUMBER: 60/090678 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090690 APPLICATION NUMBER: 60/090695 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090863 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091978 FILLING DATE: 1998-07-07 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 969060/09 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091626 FILING DATE: 1998-07-02 60/090694 APPLICATION NUMBER: 60/091519 APPLICATION NUMBER: 60/091633 FILING DATE: 1998-07-02 APPLICALL...
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APPLICATION NUMBER: 60/0
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APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089653
FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088167
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-19
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                                                                                                        Gaps
                                                 .Length 206;
                                                                                                     Indels
                                                 Score 113.5; DB 9
Pred. No. 8.1e-08;
                                                                                                   7; Mismatches
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                                                                                                                                                                               Sequence 403, Application US/09993687 Publication No. US20020198149A1 GENERAL INFORMATION:
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APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
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FILING DATE: 1998-06-03
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A
                                               Query Match 61.4%;
Best Local Similarity 66.7%;
Matches 22; Conservative
; PRIOR FILING DATE: 1998-07-09
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Gerritsen, Mary E.
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Godowski, Paul
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Query Match
61.4%; Score 113.5; DB 9; Length 206;
Best Local Similarity 66.7%; Pred. No. 8.1e-08;
Matches 22; Conservative 7; Mismatches 3; Indels 1
PRIOR FILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-22
PRIOR FILING DATE: 1998-06-22
PRIOR FILING DATE: 1998-06-22
PRIOR PAPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR PAPLICATION NUMBER: 60/090359
PRIOR FILING DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-23
PRIOR FILING DATE: 1998-06-24
PRIOR PRIOR DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09069
PRIOR FILING DATE: 1998-06-25
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PRIOR PLING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-26-26
PRIOR PILING DATE: 1998-0
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APPLICATION UNMBER: 60/090252
FILING DATE: 1998-06-25
APPLICATION NUMBER: 60/090254
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FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/989,734
CURRENT FILING DATE: 2001-11-19
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PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/065186
PRIOR PELING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR PELING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/076910
PRIOR PELING DATE: 1998-03-26
PRIOR PELING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
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FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/088028
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Williams, P. Mickey
Wood, William I.
                                                                               Ferrara, Napoleone
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Botstein, David
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088326
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LICATION NUMBER: 60/088810
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PPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/089908
FILING DATE: 1998-06-18
 APPLICATION NUMBER: 60/088030
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APPLICATION NUMBER: 60/088033
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FILING DATE: 1998-06-05
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ILING DATE: 1998-06-10
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PPLICATION NUMBER: 60/088824
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LING DATE: 1998-06-11
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3 DATE: 1998-06-12
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APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089532
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089907
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PLICATION NUMBER:
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Gaps 1; Length 206; Indels DB 9; Score 113.5; DB 9 Pred. No. 8.1e-08, 7; Mismatches 5 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK 36 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24 APPLICATION DATE: 1998-06-20
APPLICATION NUMBER: 60/091360
APPLICATION NUMBER: 60/091360
APPLICATION NUMBER: 1998-07-01 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILING DATE: 1998-07-09 APPLICATION NUMBER: 60/090445 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090678 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/091519 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091978 FILING DATE: 1998-07-07 60/090355 LICATION NUMBER: 60/090431 ING DATE: 1998-06-24 APPLICATION NUMBER: 60/090435 APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-24 60/090472 60/090535 APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542 60/090557 LICATION NUMBER: 60/090676 069060/09 APPLICATION NUMBER: 60/090695 APPLICATION NUMBER: 60/090696 60/090863 APPLICATION NUMBER: 60/091478 APPLICATION NUMBER: 60/091544 APPLICATION NUMBER: 60/091626 APPLICATION NUMBER: 60/090694 61.48; 66.78; 1998-06-23 FILING DATE: 1998-06-24 1998-06-24 1998-06-24 1998-06-24 1998-06-24 1998-06-25 1998-06-26 1998-07-02 998-07-02 1998-06-25 998-07-0 1998-07-0 1998-06-2 1998-06-2 1998-06-2 Query Match 61.4 Best Local Similarity 66.7 Matches 22; Conservative LICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: LICATION NUMBER: LICATION NUMBER: FILING DATE: 1998-0 FILING DATE: : FILING DATE: FILING DATE: DATE: DATE: FILING DATE: DATE: ING DATE: FILING DATE: LLING FILING FILING FILING FILING FILING FILING ò QQ

RESULT 14 US-10-127-966-2 ; Sequence 2, Application US/10127966

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R APPLICATION NUMBER: 60/062250
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R FILING DATE: 1997-11-12
R APPLICATION NUMBER: 60/065311
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                                                   APPLICATION NUMBER: 60/049787
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-10
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                                                                                                                      TITLE OF INVENTION: Compositions and Methods for the Diagnosis and TITLE OF INVENTION: Compositions and Methods for the Diagnosis and TITLE OF INVENTION: Treatment of Tumor TITLE OF INVENTION: Treatment of Tumor CURRENT ED204R1: 2002-04-23 CURRENT APPLICATION NUMBER: US/10/127,966 CURRENT FILING DATE: 1002-04-23 PRIOR PILING DATE: 1999-08-18 PRIOR APPLICATION NUMBER: PCT/US99/1252 PRIOR FILING DATE: 1999-06-02 PRIOR FILING DATE: 2000-03-30 PRIOR FILING DATE: 2000-03-30 PRIOR FILING DATE: 2001-02-28 PRIOR FILING DATE: 2001-11-14 PRIOR FILING DATE: 2001-11-14
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61.4%: Score 113.5; DB 9;
Best Local Similarity 66.7%; Pred. No. 8.1e-08;
Matches 22; Conservative 7; Mismatches 3;
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TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC38
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Publication No. US20030008297A1
GENERAL INFORMATION:
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Gurney,Austin L.
 No. US20030003507A1
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Stewart, Timothy A
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Goddard, Audrey
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                                                       Eaton, Dan L.
Goddard, Audrey
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Desnoyers, Luc
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US-10-127-966-2
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APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
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ILING DATE: 1998-06-19
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FILING DATE: 1998-06-19
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ILING DATE: 1998-06-22
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FILING DATE: 1998-06-23
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PPLICATION NUMBER: 60/090694
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FILING DATE: 1998-06-25
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PRIOR PILING DATE: 1998-06-25 PRIOR PILING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/090863 PRIOR PAPLICATION NUMBER: 60/090863 PRIOR PAPLICATION NUMBER: 60/090863 PRIOR PILING DATE: 1998-06-26 PRIOR PILING DATE: 1998-06-26 PRIOR FILING DATE: 1998-07-02 PRIOR PAPLICATION NUMBER: 60/091544 PRIOR APPLICATION NUMBER: 60/091544 PRIOR PILING DATE: 1998-07-02 PRIOR PILING DATE: 1998-07-02 PRIOR PILING DATE: 1998-07-02 PRIOR PELING DATE: 1998-07-02 PRIOR PELING DATE: 1998-07-02 PRIOR PELING DATE: 1998-07-07 P		Gaps	
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Sequence 99, Appl Sequence 25686, A Sequence 25, Appl Sequence 2, Appl Sequence 2, Appl

Sequence 403, App Sequence 10, Appl

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403, 403, 403,

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CS 09-791-537-25686

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CS 09-705-238-403

CS 09-989-723-403

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42, Appl
62196, A
37, Appl
41, Appl
145359,
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                         version 5.1.4_p5_4578 - 2003 Compugen Ltd.
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1 SKSGKGKDDIRNEIDKLWREVNSLKEMQALQTVCLK
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                                                                                                                                               protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
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Pred. No. 4.7e-09;
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TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE PEFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT APPLICATION NUMBER: US 60/264,022
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR PLICATION NUMBER: DK PA2001 00057
PRIOR PLICATION NUMBER: DK PA2000 01682
PRIOR FILING DATE: 2001-01-15
                                                                                                                                   APPLICANT: LATEGO, INGTIG. KJOLLEY
TITLE OF INVENTION: Trimerising module
FILE REFERENCE: THOGERSEN - 1
CURRENT APPLICATION NUMBER: US/09/445,576
CURRENT FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: PCT/DK98/00245
PRIOR PLING DATE: 1998-06-11
PRIOR PLING DATE: 1997-06-11
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 124.5;
                                                         Holtet, Thor Las
Graversen, Niels Jonas Heilskov
Kastrup, Jette Sandholm
Nielsen, Bettina Bryde
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4 KEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
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US-09-987-107-41
Sequence 41, Application US/09987107
GENERAL INFORMATION:
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nilarity 72.7%;
Conservative
                                             Michael
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SOFTWARE: Patentin version 3.1
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1 Similarity 72.7%;
24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Josepl
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Best Local Similarity
Matches 24; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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LENGTH: 36
                                                                                                                     APPLICANT:
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LENGTH: 36
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                                                                                                    APPLICANT
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bancer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY: MEMBE
FILE REFERENCE: 261/210
                  ö
                  Gaps
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              Indels
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3.2e-17;
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                                                                                                                                                   US-09-987-107-42

Sequence 42, Application US/09987107

GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
APPLICANT: MOESTRUP, Soren.
TITLE OF INVENTION: APPLIPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA BORDENIA APPLICATION WUNBER: US/09/987,107
CURRENT APPLICATION NUMBER: US 60/264,022
PRIOR PILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-01-26
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR PILING DATE: 2001-01-15
PRIOR PELICATION NUMBER: DK PA2000 01682
PRIOR FILING DATE: 2000-11-10
SOFTWARR: PALECATION NUMBER: DK PA2000 01682
SEQ ID NO 42 SEQ ID NOS: 91
FEATURE PILING DATE: 2000-11-10
                                                             1 SKSGKGKDDLRNEIDKLWREVNSLKEMQALQTVCLK 36
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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US-09-987-107-42
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; ORGANISM: Carcharhinus springeri
US-09-791-537-62196
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      Conservative
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Best Local Similarity
Matches 36; Conserv
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LENGTH: 166
    36;
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US-09-445-576-37
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Matches
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Sequence 99, Application US/09346327
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                   DB 16; Length 197;
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Pred. No. 1.2e-06;
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                                                                                                                                                   61.4%; Score 113.5; 66.7%; Pred. No. 1.2
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Pred. No. 1.2
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    SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 99 LENGTH: 197
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CURRENT APPLICATION NUMBER: US/09/346,327
CURRENT FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 107
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66.78;
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66.78;
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Best Local Similarity 66.7
Matches 22; Conservative
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Best Local Similarity 66.7
Matches 22; Conservative
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US-09-687-507-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapien US-09-346-327-99
                                                                  TYPE: PRT
ORGANISM: Homo sapien
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SOFTWARE: FastSEQ for
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Matches 22; Conserv
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LENGTH: 197
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LENGTH: 197
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                                                                                                                                                     Query Match
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TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
FILE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038PC
CURRENT FILING DATE: 2002-06-21
CURRENT FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR PRILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-14
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APPLICANT: Xu, Jiangchun
APPLICANT: XL, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.446C3
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Pred. No. 3.8e-08;
5; Mismatches 2; Indels 1;
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Pred. No. 1.2e-06;
                                                                                                                                                                                                                                                                                              6; Mismatches
TITLE OF INVENTION: METHODS OF USE THEREOF; FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
LENGTH: 197
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SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 99, Application US/09288950
; GENERAL INFORMATION:
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66.78;
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Best Local Similarity 72.7%;
Matches 24; Conservative
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US-09-791-537-145359
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Best Local Similarity
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PCT-US02-19669-55
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LENGTH: 197
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Gaps

Length 197;

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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin Version 3.0
FEW ID NO 25686
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APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
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                                                                                                                                                                                                             DB 21;
                                                                                                                                                                                                     Query Match 61.4%; Score 113.5; DB 21; Best Local Similarity 66.7%; Pred. No. 1.2e-06; Matches 22; Conservative 7; Mismatches 3;
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Pred. No. 1.2e-06;
7; Mismatches 3
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CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 99
LENGTH: 197
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
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Zhao, Xumei
Gannavarpu, Manjula
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Best Local Similarity 66.7%;
Matches 22; Conservative
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Mertens, Maureen
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Hoersch, Sebastian
Monahan, John
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Bast Jr., Robert
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Wang, Youzhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-25686
                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-381-99
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APPLICANT: Xu, Janagohun
APPLICANT: Xu, Janagohun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.446D1
FURBUT APPLICATION NUMBER: US/09/745,288
NUMBER OF SED ID NOS: 101
SOFTWARE FILENCE AND MOSTE: 2000-12-19
NUMBER OF SED ID NOS: 101
SOFTWARE FASTERO for Windows Version 3.0
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                                                                                                                                     APPLICANT: Dillon, Davin C.
APPLICANT: Ester, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY.
TITLE OF INVENTION: AND DIRACNOSIS OF BREAST CANCER
TITLE REFERENCE: 210121 446C6
CURRENT FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 99
LENGTH: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Harlocker, Susan L. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER FILE REFERENCE: 210121.44667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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1.2e-06;
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66.7%; Pred. No. 1.20
ive 7; Mismatches
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66.7%; Pred. No. 1.2¢
tive 7; Mismatches
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APPLICANT: Reed, Steven G.
APPLICANT: Xu, Jiangchun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 99, Application US/09745288 GENERAL INFORMATION:
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Best Local Similarity 66.74
Matches 22; Conservative
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Retter, Marc W.
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Best Local Similarity 66.79
Matches 22; Conservative
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; ORGANISM: Homo saplen
US-09-687-507A-99
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ORGANISM: Homo sapien
US-09-745-288-99
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US-09-778-381-99
; Sequence 99, Applica
; GENERAL INFORMATION:
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Search completed: April 15, 2003, 12:04:11 Job time : 184 secs

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Best Local Similarity
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LENGTH: 36
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LENGTH: 36
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24, Appl
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241.276 Million cell updates/sec
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403,
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                                                                                                              April 15, 2003, 11:48:39; Search time 23.25 Seconds
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US-09-445-576A-39

US-09-289-73-403

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US-01-125-923A-276

US-10-125-923A-276

US-10-125-923-64

US-10-174-575-276

US-10-174-575-276

US-10-197-75-276

US-10-199-67-276

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US-10-199-67-276

US-09-445-576A-37

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US-09-445-576A-13

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US-09-999-570-62

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GenCore version
Copyright (c) 1993 - 2003
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Listing first 45 summaries

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Sequence 60582,
Sequence 60583,
Sequence 60559,
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US-09-724-676-60581
US-09-724-676-60582
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US-09-724-676A-60583
US-09-724-676-60559
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; Pred. No. 7.5e-20;
0; Mismatches 0;
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                                US-09-445-576A-6
US-09-445-576A-26
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Sequence 38, Application US/09445576A
Sequence 38, Application US/09445576A
GENERAL INFORMATION:
SAPELICANT: BOTHOR PRIME A/S
TITLE OF INVENTION: Trimerising module
FILE REFERENCE: 62032.000004
CURRENT APPLICATION NUMBER: US/09/445,576A
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Borean Pharma A/S
TITLE OF INVEWTION: Trimerising module
FILE REFERENCE: 62032.000004
CURRENT APPLICATION NUMBER: US/09/445,576A
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                 Sequence 39, Application US/09445576A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
100.0%;
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Best Local Similarity 100.
Matches 36; Conservative
                                                                                                         331
592
1040
230
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ij

Gaps

ä

Length 36;

DB 5;

Score 124.5; DB 5; Pred. No. 4.5e-11; 6; Mismatches 2;

Gaps

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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                                                    Indels
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                 66.7%; Pred. No. 1.4e-08; ive 7; Mismatches 3;
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Pred. No. 1.4e-08;
; Mismatches 3;
                                                                                                                                   5 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK 36
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CURRENT APPLICATION NUMBER: US/09/989,733
CURRENT FILING DATE: 2001-11-01
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PRIOR PELING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PILING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-24
PRIOR FILING DATE: 1998-02-25
PRIOR PELING DATE: 1998-02-25
PRIOR PELING DATE: 1998-03-20
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-05-07
                                                                                                                                                                                                                                                                                          Sequence 403, Application US/09989733 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/062250
FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/065186
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Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Timothy A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roy, Margaret Ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91-90-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gerritsen, Mary E. Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paoni, Nicholas F.
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              Best Local Similarity 66.7
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ashkenazi, Avi J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kljavin, Ivar J
                                                                                                                                                                                                                                                                                                                                                                                                            Botstein, David
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Best Local Similarity 66.7
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fong, Sherman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-989-733-403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                                                                 APPLICANT: Milennium Pharmaceuticals, Inc. et al.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
CURRENT APPLICATION NUMBER, PCT/US02/19669A
CURRENT FILING DATE: 2001-06-21
PRIOR PRICATION NUMBER: US 60/299,887
PRIOR PAPLICATION NUMBER: US 60/299,887
PRIOR PLICATION NUMBER: US 60/301,572
PRIOR APPLICATION NUMBER: US 60/305,501
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-09-25
PRIOR PAPLICATION NUMBER: US 60/305,505
PRIOR PLICATION NUMBER: US 60/305,505
PRIOR PLICATION NUMBER: US 60/305,505
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2002-03-06
PRIOR FILING DATE: 2002-03-06
PRIOR FILING DATE: 2002-05-04
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CURRENT APPLICATION NUMBER: PCT/USO2/19669A

CURRENT FILING DATE: 2001-06-21

PRIOR FILING DATE: 2001-06-21

PRIOR FILING DATE: 2001-06-25

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-25

PRIOR FILING DATE: 2001-09-25

PRIOR PRIOR FILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-05-14

NUMBER OF SEQ ID NOS: 506

SSPOTWARE: FASLESEQ FOR WINDOWS VERSION 4.0
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Pred. No. 1.4e-08;
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Mismatches
4 KEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 RDKDGDLKTQIEKLWTEVNALKEIQALQTVCLR 70
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                                                                                                                                         Sequence 55, Application PC/TUS0219669A GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
PCT-US02-19669A-55
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PCT-US02-19669A-57
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Best Local Similařity
Matches 22; Conserv
                                                                                 RESULT 3
PCT-US02-19669A-55
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LENGTH: 197
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LENGTH: 206
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Gaps

5 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK 36

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FITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC RITLE OF INVENTION: ACIDS ENCODING THE SAME
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NUMBER OF SEQ ID NOS: 612
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Pred. No. 1.4e-
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C79
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                                                            Sequence 276, Application US/10125923A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2002-01-15
RRIOR APPLICATION UNDBER: 60/059263
RRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
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PRIOR FILING DATE: 1997-10-24
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PRIOR FILING DATE: 1997-10-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIOR FILING DATE: 1997-10-28
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                                                                                                                                                                                                                                                Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Gurney, Austin L
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                                                                                                                                                                  Goddard, Audrey
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Goddard, Audrey
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                                                                                                  : Baker, Kevin P.
: Chen, Jian
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; ORGANISM: Homo Sapien
US-10-125-923A-276
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Best Local Similarity
Matches 22; Conserv
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LENGTH: 206
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Pred. No. 1.4e
7; Mismatches
5 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK 36
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R APPLICATION NUMBER: 60/065186

PR FILING DATE: 1997-11-12

PR APPLICATION NUMBER: 60/065311

PR FILING DATE: 1997-11-13

PR APPLICATION NUMBER: 60/066770

PR FILING DATE: 1997-11-24
                                                                                                                   Sequence 403, Application US/09992643
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/083322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/062250
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FILING DATE: 1998-02-25
                                                                                                                                                                                                                                                                                                                                                                                           Srimaldi,J.Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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66.7%;
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Stewart, Timothy A
                                                                                                                                                                                                                                                                 errara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                       Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                            Surney, Austin L.
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Best Local Similarity 66.7
Matches 22; Conservative
                                                                                                                                                                               Baker, Kevin P.
Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                      (ljavin, Ivar J
                                                                                                                                                                                                                                                                                                                                                    ioddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                        Sodowski, Paul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         umas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-992-643-403
                                                                                                US-09-992-643-403
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Gaps

Length 206; Indels

.4e-08; DB 6;

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TYPE: PRT
ORGANISM: Homo Sapien
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LENGTH: 206
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LENGTH: 206
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FILE REFERENCE: P43.08.16.35.

CURRENT APPLICATION NUMBER: US/10/174,575.

CURRENT FILING DATE: 2002-01.8

PRIOR PRILING DATE: 2002-01-15.

PRIOR FILING DATE: 1997-09-18

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-24
                                                                                        CURRENT APPLICATION NUMBER: US/10/205,892
CURRENT FILING DATE: 2002-07-26
FRIOR PELICATION NUMBER: US/10/2286
FRIOR PELICATION NUMBER: 10/5286
FRIOR PELICATION NUMBER: 0/05286
FRIOR PELICATION NUMBER: 60/059263
FRIOR APPLICATION NUMBER: 60/059266
FRIOR APPLICATION NUMBER: 60/059266
FRIOR APPLICATION NUMBER: 60/06250
FRIOR FILING DATE: 1997-09-18
FRIOR PELICATION NUMBER: 60/063120
FRIOR PELICATION NUMBER: 60/063120
FRIOR APPLICATION NUMBER: 60/063121
FRIOR APPLICATION NUMBER: 60/063121
FRIOR APPLICATION NUMBER: 60/063121
FRIOR PELING DATE: 1997-10-24
FRIOR PELING DATE: 1997-10-24
FRIOR PELING DATE: 1997-10-28
FRIOR APPLICATION NUMBER: 60/063541
FRIOR APPLICATION NUMBER: 60/063541
FRIOR PELING DATE: 1997-10-28
FRIOR PELING DATE: 1997-10-28
FRIOR PELING DATE: 1997-10-28
FRIOR PELING DATE: 1997-10-28
FRIOR FILING DATE: 1997-10-28
IITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC IITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C517
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Gurney, Austin L
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Smith, Victoria
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; ORGANISM: Homo Sapien
US-10-205-892-276
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LENGIH: 206
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APPLICANT:
APPLICANT:
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APPLICANT: Zhang Zemin TITLIAN TITLIAN TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC FILE REPERENCE: P3430R1035
CURRENT APPLICATION NUMBER: U5/10/174,575A
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR PELICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR PELICATION NUMBER: 60/063260
PRIOR FILING DATE: 1997-00-17
PRIOR PELICATION NUMBER: 60/063120
PRIOR PILING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/063121
PRIOR PELICATION NUMBER: 60/063121
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-10-28
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PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR PLILING DATE: 1997-10-24
PRIOR PLILING DATE: 1997-10-21
PRIOR PILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-28
PRIOR PLILOR APPLICATION NUMBER: 60/063541
PRIOR PLILOR DATE: 1997-10-28
PRIOR PILING DATE: 1997-10-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
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Pred. No. 1.4e-08;
7; Mismatches 3,
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66.7%;
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Best Local Similarity 66.73
Matches 22, Conservative
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US-10-174-575-276
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/063486
PRIOR PELING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR PELING DATE: 1997-10-28
PRIOR RAPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
PRIOR FILING DATE: 1997-10-28
REMAINING PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
REMAINING PRIOR APPLICATION DATE: 1997-10-28
REMAINING PRIOR SEO ID NOS: 612
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1.4e-08;
                                                                                                                                                                                                                                                                 TILLE OF INVENTION ACIDS ENCOURTHE SAME
FILE REFERENCE: P4430R1C1
CURRENT PAPELICATION NUMBER: US/10/187,749
CURRENT FILING DATE: 2002-07-01
PRIOR PAPELICATION NUMBER: US/10/052,586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/05250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063250
PRIOR PAPELICATION NUMBER: 60/063120
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
                                                                                                                                                                         Watanabe, Colin K.
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                                                                             Godowski, Paul J. Gurney, Austin L.
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Gurney, Austin L
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Matches 22; Conservative
                                                                                                                                                                                                     Wood, William I.
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan,James
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US-10-199-672-276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFREENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/187,755
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: (0/059263
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-28
                                                                                                    Gaps
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                                                                                                    1;
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                                                   Length 206;
                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6;
                                                   DB 6;
                                                                             .4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
                                                                                               7; Mismatches
                                                   Score 113.5;
Pred. No. 1.4
                                                                                                                                                                         Score 113.5;
Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 KGKD-DLRNEIDKLWREVNSLKEMQALQTVCLK 36
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US-10-187-749-276
Sequence 276, Application US/10187749
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      Sequence 276, Application US/10187755 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61.48;
66.78;
                                              Query Match 61.4%;
Best Local Similarity 66.7%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Godowski, Paul J. Gurney, Austin L.
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Best Local Similarity 66.7
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      Desnoyers, Luc
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo Sapien
US-10-187-755-276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pan, James
US-10-174-575A-276
                                                                                                                                                                                                                                                                      RESULT 11
US-10-187-755-276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 276
LENGTH: 206
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Gaps

Gaps

1;

Length 206; Indels

1.5; DB 6; 1.4e-08; ches 3;

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PRIOR FILING DATE: 1997-10-20

PRIOR APPLICATION NUMBER: 60/063544

PRIOR FILING DATE: 1997-10-28

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 276

LENGTH: 206
                                                                                                                                                                                                                                                                                                                                                                                     Score 113.5; I
Pred. No. 1.4e-
7; Mismatches
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Job time : 24.25 secs
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66.78;
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Matches 22; Conservative
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CRGANISM: Homo Sapien
US-10-194-486-276
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Best Local Similarity
Matches 20; Conserv
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                                           PRIOR FLILING DATE: 1997-09-18
PRIOR FLILING DATE: 1997-09-18
PRIOR FLILING DATE: 1997-09-18
PRIOR FLILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-10-17
PRIOR PLICATION NUMBER: 60/063120
PRIOR PLICATION NUMBER: 60/063121
PRIOR PLICATION NUMBER: 60/063121
PRIOR PLICATION NUMBER: 60/063121
PRIOR PLICATION NUMBER: 60/063486
PRIOR PLING DATE: 1997-10-24
PRIOR PLING DATE: 1997-10-28
PRIOR PLING DATE: 1997-10-28
PRIOR PLING DATE: 1997-10-28
PRIOR PLING DATE: 1997-10-28
PRIOR PLICATION NUMBER: 60/063541
PRIOR PLICATION NUMBER: 60/063541
PRIOR PLICATION NUMBER: 60/063544
PRIOR PLICATION NUMBER: 60/063544
PRIOR PLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
PRIOR PLICATION NUMBER: 60/063544
PRIOR PLICATION N
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CURRENT APPLICATION NUMBER: US/10/194,486
CURRENT FILING DATE: 2002-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 1.4e-08;
7; Mismatches 3
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PRIOR APPLICATION NUMBER: US/10/052,586
PRIOR FILING DATE: 2002-01-15
PRIOR FILING DATE: 1002-01-15
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR APPLICATION NUMBER: 60/05926
PRIOR APPLICATION NUMBER: 60/05250
PRIOR FILING DATE: 1997-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 276, Application US/10194486 GENERAL INFORMATION:
                                 60/059263
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PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
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PRIOR FILING DATE: 1997-10-28
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PRIOR FILING DATE: 1997-10-21
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66.7%;
FILING DATE: 2002-01-15
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Wood, William I.
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Best Local Similarity 66.7°
Matches 22; Conservative
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Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-199-672-276
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US-10-194-486-276
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Gaps
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0
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US-09-445-576A-37
Sequence 37, Application US/09445576A
Sequence 37, Application US/09445576A
SERVERAL INFORMATION:
APPLICANT: Borean Pharma A/S
TITLE OF INVENTION: Trimerising module
FILE REFERENCE: 62032.000004
CURRENT APPLICATION UNMBER: US/09/445,576A
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PATENTIN VERSION 3.1
SEQUENCE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 SGKGKDDLRNEIDKLWREVNSLKEMQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SSKWFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
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version 5.1.4_p5_4578 - 2003 Compugen Ltd.
 GenCore
Copyright (c) 1993
```

OM protein . protein search, using sw model

Run on:

April 15, 2003, 11:45:44; Search time 11.75 Seconds (without alignments) 294.540 Million cell updates/sec

US-09-445-576A-39 185 Title: Perfect score:

1 SKSGKGKDDLRNEIDKLWREVNSLKEMQALQTVCLK 36 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	tetranectin homolo	, tetranectin precur		transmembrane effl	keratin 8, type II	translation elonga	heat shock transcr		heat shock transcr	hypothetical prote	puff-specific nucl	Na+/K+-exchanging	P63 protein - huma	heat-shock protein	conserved hypothet	hypothetical prote		hypothetical prote	_	. hypothetical prote	hypothetical prote		್ತಾ	hypothetical prote	formyltetrahydrofo	activation/secreti	transcription fact	. Na+/K+-exchanging	variant-specific's
	,	ID	A37289	JC4031	TTHUN	D81379	S05474	B70389	S52751	A40583	A41137	F75216	A56575	B37227	S33377	JC4199	F90072	T32623	JC7112	S34019	B90230	T27508	T19539	T19542	T51890	S57536	H89957	T43071	159340	0	T28432
		DB	-	~	-	7	7	7	7	7	~	~	~	~	~	N	~	~	~	~	~	~	7				7		7	, ,	7
		Length	166	202	202	1040	489	582	448	503	. 529	281	547	1010	601	451	635	654	164	123	232	069	614	627	1844	102	555	559	589	1013	3078
æ	Query	Match	100.0	48.1	45.4	33.0	32.7	31.9	30.8	30.8		30.3	30.3	30.3			29.7	29.7	29.5	29.5	29.5	29.5	28.9	28.9	28.9	28.6	28.6	٠		28.6	28.6
		Score	185	89	84	61	60.5	29	57	57		26		n	55.5	22	22	2	54.5	54	24	54	53.5	53.5			53			53	23
	Result	No.	1	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21		23 -	24	25	26	27	28	29

a role in invasive cancer.

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Gaps

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Query Match 48.1%; Score 89; DB 2; Length 202; Best Local Similarity 58.8%; Pred. No. 0.00082; Matches 20; Conservative 5; Mismatches 9; Indels

ribosomal protein	hypothetical prote	ribosomal protein	protein Fl3E6.1 [i	sensor histidine k	heat shock transcr	citron - mouse	hypothetical prote	desmoplakin I - hu	replicative DNA he	casp homolog - fis	hypothetical prote	transmembrane prot	26S proteasome req	carbonate dehydrat	
S73170 B69465	D83769	S78375	E89632	G72415	A36295	S68420	S48385	A38194 '	865970	T41332	90996н	AG1739	S48369	S10200	
77	4 (7	7	7	7	-	7	7	7	~	7	7	7	7	٦	
241	156	. 229	257	285	691	1597	1679	2677	454	633	889	927	945	328	
28.4	28.1	28.1	28.1	28.1	28.1	28.1	28.1	28.1	27.8	27.8	27.8	27.8	27.8	27.6	
52.5	25	52	52	52	52	52	52	52	51.5	51.5	51.5	51.5	51.5	. 51	
30	32	33	34	35	36	37	38	36	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1

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C. Species: Carcharhinus springeri (reef shark)
C. Accession: A37289; A37287
C. Accession: A37289; A37289
C. Aritle: Primary Structure of a protein isolated from reef shark Carcharhinus springe A; Reference number: A37289; MUID:93284081; PMID:1304877
A, Accession: A37289
A, Molecule type: protein
A; Residues: 1-166 <NE2>
C. Superfamily: tetranectin; C-type lectin homology
C; Superfamily: tetranectin; C-type lectin homology
C; Keywords: cartilage
F; 37-47, 64-160, 136-152/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C. Accession: JC4031
R. Sorensen, C. B.; Berglund, L.; Petersen, T.E.
Gene 132, 243-245, 1995
A.Title: Cloning of a cDNA encoding murine tetranectin.
A.Reference number: JC4031; MUID:95137396; PMID:7835708
A.Accession: JC44031
A.Molecule type: mRNA
A.Residues: 1-202 <SOR>
A.Cross-references: EMBL:X79199; NID:g671561; PIDN:CAA55791.1; PID:g671562
A.Experimental source: lung
C.Comment: This protein binds plasminogen, and may play a role in invasive canc C.Superfamily: tetranectin, C-type lectin homology
F:1-21/Domain: signal sequence #status predicted <SIG>F:22-202/Product: tetranectin #status predicted <MAT>
F:71-197/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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100.0%; Score 185; DB 1;
Best Local Similarity 100.0%; Pred. No. 6.5e-16;
Matches 36; Conservative 0; Mismatches 0;
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Gaps

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Length 1040; Indels

5 DB 15;

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A; Molecule type: DNA_A; Residues: 1-1040 <PRR>A; Residues: 1-1040 <PRR>A; Residues: 1-1040 <PRR>A; Cross-references: GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB74202.1; PID:g696 A; Experimental source: serotype O2, strain NCTC 11168 C; Genetics: A; Gene: Cj0366c A; Cross-references: Cj0366c C; Superfamily: acriflavin resistance protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               keratin 8, type II, cytoskeletal - mouse
N.Alternate names: cytokeratin A: endo A cytokeratin
N.Alternate names: cytokeratin A: endo A cytokeratin
C.Species: Mus musculus (house mouse)
C.Species: Was musculus (house mouse)
C.Species: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 10-Dec-1999
C.Scession: S0474; JT0328
R.Semat, A.; Vasseur, M.; Maillet, L.; Brulet, P.; Darmon, Y.M.
Differentiation 37, 40-46, 1988
A.Title: Sequence analysis of murine cytokeratin endo A (no 8) cDNA. Evidence for mRN
A.Reference number: S05474; MUID:88255624; PMID:2454862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Molecule type: DNA
A:Residues: 1-489 <SEM>
A:Residues: 1-489 <SEM>
A:Cross-references: EMBL:X12789; NID:952788; PIDN:CAA31278.1; PID:952789
A:Cross-references: EMBL:X12789; NID:952789; NID:952789; NID:952789; NID:952789; NID:952789; NID:95277; NID:95278; NID:95277; NID:95278; NID:95278; NID:95278; NID:95278; NID:95278; NID:95278; NID:95278; MID:95218; NID:95218; MID:95218; MID:95218; MID:95218; MID:95278; MID:9528; MID:95218; MID:9528; MID:
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A;Reference number: A70300; MUID:98196666; PMID:9537320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 02-Feb-2001
C;Accession: B70389
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A; Cross-references: GB:M21836
C; Superfamily: cytoskeletal keratin
C; Keywords: colled coll; intermediate filament
E; 1-96/Domain: head <HED>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Mismatches
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681 NKSGKSYDEIQKDVNKLVAVANQRKELSRVRT 712
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 61;
Pred. No.
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ilarity 34.4%;
Conservative 1
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Best Local Similarity 43.8
Matches 14; Conservative
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F;266-403/Region: coil 2
F;404-489/Domain: tail <TAI>
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:97-403/Domain: rod <ROD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150-241/Region: coil 1B
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                                      preliminary
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R;Wever, U.M.; Albrechtsen, R.
Lab. Invest. 67, 253-262, 1992
A;Title: Tetranectin, a plasminogen kringle 4-binding protein. Cloning and gene expressi
A;Reference number: A56835; MUID:92365345; PMID:1354271
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Blochemistry 26, 6757-6764, 1987
A;Title: Primary structure of tetranectin, a plasminogen kringle 4 binding plasma protei
A;Reference number: A29747; MUID:88107595; PMID:3427041
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R; Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypa: A;Reference number: A81250; MUID:20150912; PMID:10688204
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C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
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Accession: S24126; A56835; A29747; I38359; S19865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The gene structure of tetranectin, a plasminogen binding protein. A;Reference number: S24126; MUID:92380263; PMID:1511740
A;Accession: S24126
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Residues: 1-202 <WEW>
Cross-references: EMBL:X64559; NID:g37408; PIDN:CAA45860.1; PID:g37409
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C.Keywords: glycoprotein; plasma; tetraner
F.1-21/Domain: signal sequence #status predicted <SIG>
F.22-202/Product: tetranectin #status experimental <MAT>
F.71-197/Domain: C-type lectin homology <LCH>
F.75/Binding site: carbohydrate (Thr) (covalent) #status experimental
F.71-81,98-197,173-189/Disulfide bonds: #status experimental
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45.4%; Score 84; DB 1; Length 202;
Best Local Similarity 58.6%; Pred. No. 0.0035;
Matches 17; Conservative 6; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                              tetranectin precursor (validated) - human
N;Alternate names: plasminogen-kringle 4 binding protein
                                               SGKGKDDLRNEIDKLWREVNSLKEMQALQTVCLK 36
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A,Residues: 22-105,'G',107-202 <FUH>
A:Experimental source: plasma
A;Note: 55-Ser and 58-Met were also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Experimental source: placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berglund, L.; Petersen, T.E.
EBS Lett. 309, 15-19, 1992
                                                                                                                                                                                                                                                                                                                                                                        Species: Homo sapiens (man)
Date: 30-Jun-1992 #sequence
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A; Introns: 37/1; 70/1
C; Complex: homotetramer
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A; Residues: 1-202 <BER>
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A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA

A; Accession: B70389

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C; Accession: A41137
R; Rabindran, S.K.; Glorgi, G.; Clos, J.; Wu, C.
R; Rabindran, S.K.; Glorgi, G.; Clos, J.; Wu, C.
Rytile: Molecular cloning and expression of a human heat shock factor, HSF1.
A; Reference number: A41137; MUID:9134376; PMID:1871105
A; Residues: A41137; MUID:9134376; PMID:1871105
A; Rocession: A41137
A; Molecule type: MRNA
A; Residues: 1-529 cRAB>
A; Cross-references: GB:M64673; NID:9184402; PIDN:AA52695.1; PID:9184403
A; Cross-references: GDB:128783; OMIM:140580
A; Gene: GDB:HSF1
A; Cross-references: GDB:128783; OMIM:140580
A; Map position: 8924.3-8924.3
C; Superfamily: tomato heat shock transcription factor HSF8; HSF DNA-binding domain ho C; Superfamily: Lomato heat shock transcription regulation
F; 18-124/Domain: HSF DNA-binding domain homology <HSF>
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C;Species: Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: F75216
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s A;Reference number: A75001
A;Accession: F75216
A;A
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puff-specific nuclear protein Bx42 - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jul-2000

C;Accession: A56575

R;Wielland, C.; Mann, S.; von Besser, H.; Saumweber, H.

Chromosoma 101, 517-525, 1992

A;Title: The Drosophila nuclear protein Bx42, which is found in many puffs on polyten
A;Reference number: A56575; MUID:93048378; PMID:1424996
                                                                                                                               A41137
heat shock transcription factor 1 - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Mar-2000
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Pred. No. 23;
7; Mismatches
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16;
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Pred. No.
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50.0%;
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Best Local Similarity 37.1%;
Matches 13; Conservative
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Best Local Similarity
Matches 11; Conserv
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                                                                                            RESULT 9
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C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Species: Obj. 1992 #sequence_revision 05-Jun-1992 #text_dhange 19-May-2000
C:Accession: A40583
A:Starge, K.D.; Zimarino, V.; Holm, K.; Wu, C.; Morimoto, R.I.
Genes Dav. 5, 1902-1911, 1991
A:Title: Cloning and characterization of two mouse heat shock factors with distinct indu A:Reference number: A40583 MUID:92009180; PMID:1717345
A:Accession: A40583
A:Status: preliminary
A:Molecule type: mRNA
A:Molecule type: mRNA
A:Residues: 1-503 <SAR>
A:Coss-references: GB:X61753; NID:951445; PIDN:CAA43892.1; PID:951446
C:Superfamily: tomato heat shock transcription factor HSF8; HSF DNA-binding domain homol C:Keywords: DNA binding; transcription regulation
F:18-124/Domain: HSF DNA-binding domain homology <HSF>
A.Molecule type: DNA
A.Residues: 1-582 <AQF>
A.FOROSE-references: GB-AE000719; NID:92983517; PIDN:AAC07099.1; PID:92983523; GB:AE00065
A.Fenerimental source: strain VF5
C.Genetics:
A.Gene: selB
A.Gene: SelB
C.Superfamily: translation elongation factor selB; translation elongation factor Tu homc
C.Reywords: GTP binding; nucleotide binding; P-loop
F:4-119/Domain: translation elongation factor Tu homology <ETU>
F:10-17/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X83094; NID:9758270; PIDN:CAA58149.1; PID:9758271
C;Superfamily: tomato heat shock transcription factor HSF8; HSF DNA-binding domain homol
F:1-47/Domain: HSF DNA-binding domain homology (fragment) <HSF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Riswanynathan, S.K.; Revathl, C.J.; Srinivas, U.K.
submitted to the EMBL Data Library, November 1994
A;Description: Cloning and characterization of rat heat shock transcription factor 1.
A;Reference number: $52751
A;Accession: $52751
A;Accession: Liminary
A;Molecule type: mRNA
A;Residues: 1-448 <SWA>
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heat shock transcription factor HSF1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_dhange 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Species: Rattus norvegicus (Norway rat)
Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heat shock transcription factor 1 - rat (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SGKGKDDLRNEIDKLWREVNSLKEMQALQ 31
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37.9%;
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ilarity 37.1%;
Conservative
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37.1%;
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Best Local Similarity
Matches 13; Conserv
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Accession: \$52751

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A; Accession: A56575

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JC4199
heat-shock protein 1 - African clawed frog
C:Species: Kenopus laevis (African clawed frog)
C:Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 21-Jul-2000
C:Accession: JC4199
R:Stump, D.G.; Landsberger, N.; Wolffe, A.P.
Gene 160, 207. 211, 1995
A:Title: The CDNA encoding Xenopus laevis heat-shock factor 1 (XHSF1): nucleotide and A;Reference number: JC4199; MUID:95365690; PMID:7642097
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Job time : 12.75 secs
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Best Local Similarity 37.9
Matches 11; Conservative
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A; Residues: 1-1010 <TAZ>
A; Residues: 1-1010 <TAZ>
A; Residues: 1-1010 <TAZ>
A; Residues: 1-1010 <TAZ>
A; Cross-references: GB:M59960; NID:g212407; PIDN:AAA48982.1; PID:g212408.
C; Superfamily: Na+/K+transporting Arpase alpha chain; ArPase nucleotide-binding domain
C; Reywords: ATP; glycoprotein; hydrolase; phosphoprotein; potassium transport; sodium tr
F; 574-770/Domain: Arpase nucleotide-binding domain homology <ARNS
F; 502,470/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 363/Active site: Asp (aspartylphosphate intermediate) #status predicted
F; 495/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 13-3m-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Accession: S33377
R;Schweizer, A.; Rohrer, J.; Jenoe, P.; DeMaio, A.; Buchman, T.G.; Hauri, H.P.
C;Accession: Scil 104, 685-694, 1993
A;Telle: A reversibly palmitoylated resident protein (p63) of an ER-Golgi intermediate A;Accession: S33377, MUID:93300949; PMID:8314870
A;Wolecule type: DNA
A.Residues: 1-547 <WIE>
A.Cross-references: GB:X64536, GB:S48763; NID:98391; PIDN:CAA45834.1; PID:98392
A.Note: sequence extracted from NCBI backbone (NCBIN:118716, NCBIP:118718)
C;Genetics:
A:Gene: FlyBase:Bx42
A:Gene: FlyBase:Bx42
A:Cross-references: FlyBase:FBgn0004856
C;Superfamily: Caenorhabditis elegans hypothetical protein T27F2.1
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                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 62;
5; Mismatches 12
                                                                                                                                                                                                                                       Score 56; DB 2;
Pred. No. 32;
3; Mismatches
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Pred. No. 41;
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                                                                                                                                                                                                                                                                                                                                                                   431 SGYGDDEAYNVYDKPWRDSNTL 452
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46.2%;
                                                                                                                                                                                                                                                          Local Similarity 50.0
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Best Local Similarity 40.0%
Matches 14; Conservative
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Best Local Similarity 46.29
Matches 12; Conservative
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A:Molecule type: mRNA
A:Residues: 1-601 <SCH>
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Matches
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tomato heat shock transcription factor HSF8; HSF DNA-binding domain ho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Staphylococcus aureus
C.Species: Staphylococcus aureus
C.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C.Accession: F90072;
C.Accession: F90072;
C.Accession: F90073;
C.Accession: F
A;Molecule type: mRNA
A;Residues: 1-451 <STU>
A;Cross-references: GB:L36924; NID:g558067; PIDN:AAA99999.1; PID:g558068
C;Comment: This factor is a competent to interact specifically with heat shock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
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A.Residues: 1-635 <KUR>
A.Cross-references: GB:BA000018; PID:g13702604; PIDN:BAB43744.1; GSPDB:GN00149
A.Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Pred. No. 50;
7; Mismatches
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8; Mismatches
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37.9%;
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Best Local Similarity 34.2%;
Matches 13; Conservative
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Scoring table:

Searched:

Minimum DB s Maximum DB s

Database

Perfect score:

Sequence:

OM protein

Run on:

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haemophilus
homo sapien
rhodobacter
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A Neame P.J., Young C.N., Treep J.T.;

Terms of a protein isolated from reef shark

Carcharhinus springeri) cartilage that is similar to the mammalian

T. C-type lectin homolog, tetranectin.";

T. C-type lectin homolog, tetranectin.";

Protein Sci. 1:161-168(1992).

T. C-type Lectin PoMAIN.

Protein Sci. 1:161-168(1992).

R. PINLARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

R. PINLARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

R. InterPro; 1PR001304; Lectin.C.

R. Pfam; PF00059; lectin.c.; 1.

R. SMART; SM00034; CLECT; 1.

R. PROSITE; PS00615; C_TYPE_LECTIN.1; 1.

R. PROSITE; PS00615; C_TYPE_LECTIN.2; 1.
                                                                                                                   sulfolobus
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-type lectin superfamily member 1 precursor (Cartilage-derived C-type LECIN).
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 rattus
                                                                                                                                                                                                                                                                                                                                                                                                                  Carcharhinus springeri (Reef shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Carcharhinidae; Carcharhinus.
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100.0%; Pred. No. 1.7e-16;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                      TETNICARSP STANDARD; PRT; 166 AA. P26258; Ol-MAY-1992 (Rel. 22, Created) Ol-MAY-1992 (Rel. 22, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Tetranectin-like protein.
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                                                                                                                 SYS_SULSO
HOFB_HAEIN
K2C7_HUMAN
MBHL_RHOCA
              POL2_GCMV
G160_MOUSE
RR2_GALSU
PSA3_SCHPO
RR42_HUMAN
YD12_METJA
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Best Local Similarity 100.8
Matches 36; Conservative
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166 AA;
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                                                                                                                 April 15, 2003, 11:44:09; Search time 6.5 Seconds
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               GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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1 SKSGKGKDDLRNEIDKLWREVNSLKEMQALQTVCLK
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TETN_HUMAN
K2C8_MOUSE
HSF1_CHICK
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HSF1_HUMAN
BX42_DROME
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HSF_XENLA
MAFF_MOUSE
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YNI6_YEAST
PT54_SACBA
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RR2_PORPU
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HSF_DROME
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YIO9_YEAST
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HSF2_HUMAN
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Maximum Match 100%
Listing first 45 summaries
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CAHC_PEA
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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Match Length
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SEQUENCE FROM N.A.

NCBI_TaxID-9606;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
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                                                                                                                                                               MEDLINE-96116955; Pubmed-8561165;
Ibbraki K., Kozak C.A., Wewer U.M., Albrechtsen R., Young M.F.,
"Mouse tetranectin: cDNA sequence, tissue-specific expression, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (Rel. 09, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tetranectin precursor (TN) (Plasminogen-Kringle 4 binding protein).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
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TETRANECTIN.

C-TYPE LECTIN.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

LT -> VI (IN REF. 2).

A -> T (IN REF. 2).

A -> R (IN REF. 2).

R -> Q (IN REF. 2).

R -> Q (IN REF. 2).

N; 639E7334D58EB04E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 AA.
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5; Mismatches
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EMBL; X98122; CAA66804.1;
HSSP; P09452; TTN3.
MGD; MG1:104540; Tna.
InterPro; IPR001304; Lectin_C.
SMART; SM00054; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.1%; Score 89; 58.8%; Pred. No. (
                                                                                                   chromosomal mapping.";
Mamm. Genome 6:693-696(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X79199; CAA55791.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22257 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lectin; Plasma; Signal
SIGNAL 1 21
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Matches 20; Conserv
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P05452;
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                               TISSUE-Cartilage;
MEDLINE-99453719; PubMed=10524194;
Neame P.J., Tapp H., Grimm D.R.;
"The cartilage-derived, C-type lectin (CLECSF1): structure of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Tetranectin precursor (TN) (Plasminogen-kringle 4 binding protein).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-TYPE LECTIN SUPERFAMILY MEMBER 1.
C-TYPE LECTIN
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                             BB924DBDDB7729A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.4%; Score 113.5; DB 1;
66.7%; Pred. No. 2.1e-07;
"Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C57BL/6 X CBA; TISSUE-Lung;
MEDLINE-95137396; Pubmed-7835708;
Socrensen C.B., Berglund L., Petersen T.E.;
"Cloning of a CDNA encoding murine tetranectin.";
Gene 152:243-245(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF077345, AAD12542.1;

EMBL, AF077344, AAD12542.1;

HSSP, POS452; HTM.

Genew, HONC:2052, CLECSF1.

InterPro; IPR001304; Lectin_C.

FAB., FF00059; lectin_C;

SMART; SM00054; CLECT; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
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Lectin; Signal

CHAIN DOMAIN SIGNAL

DISULFID DISULFID SEQUENCE DISULFID

22; Conservative

Local Similarity

Best Loca Matches

Query Match

STANDARD;

TETN_MOUSE P43025;

TETN_MOUSE RESULT 3

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SEQUENCE FROM N.A.

NCBI_TaxID-10090;

SEQUENCE FROM N.A. STRAIN-BALB/C;

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"Nucleotide sequence of mouse EndoA cytokeratin cDNA reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 17; Conserv
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P11679;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nielsen B.B., Kastrup J.S., Rasmussen H., Holtet T.L., Graversen J.H., Etzerodt M., Thoegersen H.C., Larsen I.K.;
"Crystal structure of tetranectin, a trimeric plasminogen-binding protein with an alpha-helical coiled coil.";
FEBS Lett. 412:388-396(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 66-202.
MEDLINE-98437604; PubMed-9757090;
Kastrup J.S., Nielsen B.B., Rasmussen H., Holtet T.L., Graversen J.H.,
Etzerodt M., Thoegersen H.C., Larsen I.K.;
"Structure of the C-type lectin carbohydrate recognition domain of human tetranectin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acta Crystallogr. D 54:757-766(1998).
-!- FUNCTION: Tetranectin binds to plasminogen and to isolated kringle
4. May be involved in the packaging of molecules destined for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jaquinod M., Holtet T.L., Etzerodt M., Clemmensen I., Thoegersen H.C., Roepstorff P.;
                                                                                                               [2]
SEQUENCE FROM N.A.
MEDLINE-92380263; Pubmed=1511740;
Berglund L., Petersen T.E.;
"The gene structure of tetranectin, a plasminogen binding protein.";
FEBS Lett. 309:15-19(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Homotrimer.
SUBCELLULAR LOCATION: Secreted.
MASS SPECTROMETRY: MW-20535.8; MW_ERR-2.4; METHOD-Electrospray;
                                                                                                                                                                                                                                                                                  MEDLINE-88107595; PubMed-3427041; Fuhlendorff J., Clemmensen I., Magnusson S.; Primary structure of tetranectin, a plasminogen kringle 4 binding plasma protein: homology with asialoglycoprotein receptors and
                                                              Wever U.M., Albrechtsen R.; "Tetranectin, a plasminogen kringle 4-binding protein. Cloning and gene expression pattern in human colon cancer."; Lab. Invest. 67:253-262(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Mass spectrometric characterisation of post-translational modification and genetic variation in human tetranectin."; Biol. Chem. 380:1307-1314(1999).
                                                                                                                                                                                                                                                                                                                                                                                                       Sorensen C.B., Berglund L., Petersen T.E.; "Cloning and mapping of the murine tetranectin gene."; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                   Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE, MASS SPECTROMETRY, AND VARIANT GLY-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                          SEQUENCE OF 22-202, AND VARIANTS SER-55 AND MET-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE=97398360; Pubmed=9256258;
                                                                                                                                                                                                                                                                                                                                          cartilage proteoglycan core protein.
Biochemistry 26:6757-6764(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE~Plasma;
MEDLINE~20080486; PubMed~10614823;
                                                  MEDLINE-92365345; PubMed-1354271;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-36 FROM N.A.
                                                                                                                                                                                             [3]
SEQUENCE FROM N.A.
NCBI_TaxID=9606;
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                                      rissue-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exocytosis.
                                                                                                                                                                                                                      TISSUE-Lung;
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01-0CT-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Keratin, type II cytoskeletal 8 (Cytokeratin 8) (Cytokeratin endo A).
KRT8 OR KRT2-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-89121483; PubMed-2464527;
Morita T., Tondella M.L.C., Takemoto Y., Hashido K., Ichinose Y.,
Nozaki M., Matsushiro A.;
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00041; C_TYPE_LECTIN_1; 1.
PROSITE; PS0011; C_TYPE_LECTIN_2; 1.
Lectin; Plasma; Signal; Polymorphism; Glycoprotein; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.4%; Score 84; DB 1; Length 202; 58.6%; Pred. No. 0.0011;
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2B0DCB5DF22E1AB8 CRC64;
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S -> G.
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C-TYPE LECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
                         or send an email to license@isb-sib.ch)
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EMBL; BC011024; AAH11024.1; ---
EMBL; X98121; CAA66803.1; ---
FIR; A29747, A29747.
PIR; S24126; S24126.
PIR; S24126; S24126.
PDB; 1HTN; 03-DEC-97.
PDB; 1HTN; 03-DEC-97.
PDB; 1HTN; 03-DEC-97.
PDB; 1HTN; 04-MAY-98.
MIM; 187520; ---
MIM; 187520; ----
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                                                                       EMBL; X70910; CAA50265.1;
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1198
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                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: HOMOTRIMER.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC DURING NORMAL GROWTH AND MOVES
TO THE NUCLEUS UPON ACTIVATION (BY SIMILARITY).
-! TISSUE SPECIFICITY: LOW EXPRESSION FOUND IN MOST TISSUES WITH THE EXCEPTION OF BLOOD AND LIVER. HIGHEST LEVELS ARE FOUND IN PIGMENTAL LAYER OF RETIRA AND IN THE LYMPHOBLASTOID CELL LINE MSB.
-!- DEVELOPMENTAL STAGE: EXPRESSED DURING DEVELOPMENT.
                                                                Nakai A., Morimoto R.I.;
"Characterization of a novel chicken heat shock transcription factor," Characterization of a novel chicken heat shock transcription factor, heat shock factor 3, suggests a new regulatory pathway.";
Mol. Cell. Biol. 13:1983-1997(1993).
- FUNCTION: DAM-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT SHOCK PROWOTER ELEMENTS (HES) MO ACTIVITY AND ACTIVITY WHE SEE UNLESS THE CELLS ARE HEAT SHOCKED OR TREATED WITH NONIONIC DETERGENTS. IT PRESENTS CONSTITUTIVE DNA BINDING ACTIVITY WHEN THE C-TERMINAL IS DELETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0cT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Heat shock factor protein 1 (HSF 1) (Heat shock transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMARY; SM00415; HSF; 1.
PROSITE; PS00444; HSF_DOMAIN; 1.
Transcription regulation; Unclear protein; DNA-binding; Activator; Phosphorylation; Heat shock; Multigene family.
DNA_BIND 20 125 BY SIMILARITY.
DOMAIN 135 208 HYDROPHOBIC REPEAT HR-A/B.
DOMAIN 346 371 HYDROPHOBIC REPEAT HR-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sarge K.D., Zimarino V., Holm K., Wu C., Morimoto R.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.8%; Score 57; DB 1; 37.1%; Pred. No. 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 KGKDD-----LRNEIDKLWREVNSLKEMQALQ 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L06098; -; NOT_ANNOTATED_CDS. HSSP; P22813; 1HKT.
                                                  MEDLINE-93204945; PubMed-8455593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKANSFAC; T01044; -.
INTERPO: PRO0032; HSF_DNa_bind.
INTERPO: IPR00341; HSF_ETS.
Pfam; PF00447; HSF_DNa-bind; 1.
PRINTS; PR00056; HSFDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD001788; HSF_DNA_bind; 1. SMART; SM00415; HSF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=WEHI-3;
MEDLINE=92009180; PubMed=1717345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 37.1
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC, TO1044:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSF1_MOUSE
P38532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSF1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
                   NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   οy
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01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Heat shock factor protein 1 (HSF 1) (Heat shock transcription factor 1) (HSF 3A) (HSF 3A) (HSF 1) (Heat shock transcription factor all us gallus (Chicken).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Archosauria: Aves: Neognathae; Galliformes: Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STUTTER.
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY MAPK AND CAMK2) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                            -1- SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                characteristics of the type-II keratin subfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60.5; DB 1; Length 488; Pred. No. 2.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> EA (IN REF. 2).
-> R (IN REF. 2).
9E1430800BB81523 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
QQ -> NR (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          491 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 AGKHGDDLRRTKTEISEMNRNINRLQEIEALK 329
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LINKER 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAIL.
COIL 1A.
LINKER 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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488
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366
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366
366
388 AA;
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Best Local Similarity
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P38529;
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DOMAIN
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CONFLICT
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MEDLINE-91334377; PubMed-1871106;
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P39736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
SUBUNIT: DNA-BINDING HOMOTRIMER IN STRESSED OR HEAT SHOCKED CELLS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSF1_HUMAN STANDARD; PRT; 529 AA.

Q00613;

Q1-FEB-1994 (Rel. 28, Created)

10-FEB-1994 (Rel. 28, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Heat shock factor protein 1 (HSF 1) (Heat shock transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                            OTHERWISE FOUND AS A MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC DURING NORMAL GROWTH AND MOVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSTIE; PS00434; HSF_DOMAIN; 1.
Transcription regulation; Nuclear protein; DNA-binding; Activator; Phosphorylation; Heat shock; Multigene family.
DNA_BIND 15 120 BY SIMILARITY.
DOMAIN 130 203 HYDROPHOBIC REPEAT HR-A/B.
DOMAIN 380 405 HYDROPHOBIC REPEAT HR-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-91334376; PubMed-1871105;
Rabindran S.K., Giorgi G., Clos J., Wu C.;
"Molecular cloning and expression of a human heat shock factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.8%; Score 57; DB 1; Length 503; 37.1%; Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0795ABB6FA169F7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE OF 73-79; 81-93; 97-106; 163-170 AND 337-352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 88:6906-6910(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 KGKDD-----LRNEIDKLWREVNSLKEMQALQ 31
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                                                                                                                                                                                                                                                                                     TO THE NUCLEUS UPON ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:96238; Hsfl.
InterPro; IPR000232; HSF_DNA_bind.
InterPro; IPR002341; HSF_ETS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00447; HSF_DNA bind; 1.
PRINTS; PR00056; HSFDOMAIN.
ProDom; PD001788; HSF_DNA_bind; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A40583; A40583.
HSSP; P22813; 1HKT.
TRANSFAC; T00384; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSFAC; T01525; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              503 AA;
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HSF1_HUMAN
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  RRTH REPRESENTATION OF THE PROPERTY OF THE PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGALHSAAA
                                                                                                                                                                                                                  -:- SUBUNT: DNA-BINDING HOMOTRIMER IN STRESSED OR HEAT SHOCKED CELLS, OTHERWISE FOUND AS A MONOMER.
-:- SUBCELLULAR LOCATION: CYTOPLASMIC DURING NORMAL GROWTH AND MOVES TO THE NUCLEUS UPON ACTIVATION.
-:- ALTERNATIVE PRODUCTS: 2 ISOPORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                       -i- FUNCTION: DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT SHOCK PROMOTER ELEMENTS (HSE) AND ACTIVATES TRANSCRIPTION. IN HIGHER EUKARYOTES, HSF IS UNABLE TO BIND TO THE HSE UNLESS THE CELLS ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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HYDROPHOBIC REPEAT HR-A/B.

HYDROPHOBIC REPEAT HR-C.

GKQLVHYTAQPLFILDPGSVDTGSNDLP -> AGALHSAP

WPAGPRUGHREQRPAGAV (IN SHORT ISOFORM).

MISSING (IN SHORT ISOFORM).

7350745074507C954365 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR00232; HSF_DNA_bind.
InterPro; IPR002341; HSF_ETS.
Pfam; PF00447; HSF_DNA-bind; 1.
PRINTS; PR00056; HSF_DNA_bind; 1.
SMART; SM00415; HSF_INA_bind; 1.
SMART; SM00415; HSF_I.
Transcription regulation; Nuclear protein; DNA-binding; Activator; Transcription regulation; Multigene family; Alternative splicing. DNA_BIND

15 120 BY SIMILARITY.
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophila; Drosophila.

NCBI_TaxID=7227;
Schuetz T.J., Gallo G.J., Sheldon L., Tempst P., Kingston R.E.; "Isolation of a cDNA for HSF2: evidence for two heat shock factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                   Proc. Natl. Acad. Sci. U.S.A. 88:6911-6915(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 KGKDD-----LRNEIDKLWREVNSLKEMQALQ 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 30.8%; Score 57; Best Local Similarity 37.1%; Pred. No. 3matches 13; Conservative 7; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequ
01-NOV-1997 (Rel. 35, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57260 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M64673; AAA52695.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Puff specific protein Bx42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC; T01042; -. Genew; HGNC:5224; HSF1.
MIM; 140580; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A41137; A41137.
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                                                                                                                                                                                              HEAT SHOCKED.
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SEQUENCE FROM N.A.
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MOD_RES
BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takeyasu K., Lemas V., Fambrough D.M.;
"Stability of Na(+)-K(+)-ATPase alpha-subunit isoforms in evolution.";
Am. J. Physiol. 259:CC19-CG30(1990)
-1- FUNCTION: THIS IS THE CATALYTIC COMPONENT OF THE ACTIVE ENZYME,
WHICH CATALYZES THE HYPROLYSIS OF ATP COUPLED WITH THE EXCHANGE OF
NA AND K IONS ACROSS THE PLASMA MEMBRANE. THIS ACTION CREATES THE
ELECTROCHEMICAL GRADIENT OF NA AND K, PROVIDING THE ENERGY FOR
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Sodium/potassium-transporting ArPase alpha-3 chain (EC 3.6.3.9)
(Sodium pump 3) (Na+/K+ ArPase 3) (Alpha(III)).
                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                          Score 56; DB 1; Length 547; Pred. No. 11;
                                                                                                                                                                                                                                                                                                       ASP/GLU-RICH (ACIDIC)
ASP/GLU-RICH (ACIDIC)
01399EA291C9D557 CRC64;
                                                                                                                                                                                                                                                                                        SH2-LIKE DOMAIN,
PRO-RICH,
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1010 AA
                                                                                                                                            TRANSCRIPT.
SIMILARITY: BELONGS TO THE SNW FAMILY.
                                                                                                                                                                                                                                                                                                                                                   Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                    431 SGYGDDEAYNVYDKPWRDSNTL 452
                                                                                                                                                                                                                                                  InterPro; IPR004015; SKIP_SNW.
Pfam; PF02731; SKIP_SNW; 1.
                                                                                                                                                                                                                                                                                                                                                                        3 SGKGKDDLRNEIDKLWREVNSL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1992 (Rel. 21, Created)
                                                                                                                                                                                                                                                                                                                        61156 MW;
                                                                                                                                                                                                                                                                                                                                          30.3%;
                                                                                                                                                                                                                                                                    Nuclear protein; DNA-binding.
                                                                                                                                                                                                                                   EMBL; X64536; CAA45834.1; -.
                                                                                                                                                                                                                                           FBgn0004856; Bx42.
                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                        547 AA;
                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                   CHICK
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SEQUENCE
                                                                                                                                                                                                                                            FlyBase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FYINLS, FROULL, NORMAN, TO TO THE PROSTER, FROULT, NORMAN, TICREAMS; TICRO1106; XK_ATPOSE_alp; 1.
PROSITE; PS00154; ATPASE_E, E2; 1.
Hydrolase; Sodium/potassium transport; Transmembrane; Phosphorylation; Magnesium; Metal-binding; ATP-binding; Multigene family.

OMAIN 1 74 . CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY PKA) (BY SIMILARITY)
BINDING OF PHOSPHOINOSITIDE-3 KINASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
ACTIVE TRANSPORT OF VARIOUS NUTRIENTS. CATALYTIC ACTIVITY: ATP + H(2)O + Na(+)(In) + K(+)(Out) = ADP phosphate + Na(+)(Out) + K(+)(In). SUBUNIT: COMPOSED OF THREE SUBUNITS: ALPHA (CATALYTIC), BETA
                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARIY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
(E1-E2 ATPASES). SUBFAMILY IIC.
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Pred. No. 22;
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111284 MW; 71526BC25633BFA6 CRC64;
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
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POTENTIAL.
LUMENAL (POTENTIAL).
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, P04191, 1EUL.
InterPro: IPR001757; ATPase_E1-E2.
InterPro: IPR004014; Cation_ATPase.
InterPro: IPR00454; Hgnase_Marpase.
InterPro: IPR00454; Hgnase/hydrlase.
Pfam: PF00122; E1-E2_ATPase.
Pfam: PF00689; Cation_ATPase_C;
Pfam: PF00690; Cation_ATPase_C;
Pfam: PF00690; Cation_ATPase_N; I.
PRINTS; PR00119; CATAPPASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M59960; AAA48982.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; B37227.
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Matches 14; Conserv
                                                                                                    AND GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; B37227
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RESULT 11

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NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- SUBCELLULAR LOCATION: CYTOPLASMIC. MEMBRANE-ASSOCIATED PROTEIN.
-:- ATERNATIVE PRODUCTS: 2 ISOFORMS; HIP1-1 AND HIP1-2; ARE PRODUCED BY ALTERNATIVE SPLICIAL.
-:- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED WITH THE HIGHEST LEVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION IS INVERSELY CORRELATED TO THE LENGTH OF THE POLYGLUTAMINE TRACT ADDED TO THE HUNTINGTIN PROTEIN IN HUNTINGTON
                                                                                                                                                                                                                                                                                                                                     "Genomic organization of the human HIP1 gene and its exclusion as a candidate gene in a family diagnosed with Huntington disease without CAG expansion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: BINDS HUNTINGTIN. THIS INTERACTION IS RESTRICTED TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE-20515263; PubMed=11063258; Chopra V.S., Metzler M., Rasper D.M., Engqvist-Goldstein A.E.Y., Singaraja R., Gan L., Fichter K.M., McCutcheon K., Drubin D., Nicholson D.W., Hayden M.R., "HIP12 is a non-proapoptotic member of a gene family including HIP1, an interacting protein with huntingtin."; an interacting protein with huntingtin."; —: FUNCTION: MAY PLAY A FUNCTIONAL ROLE IN THE CELL FILAMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
MEDLINE-97227296; PubMed-9147654;
WANNER E.E., Rovira C., Scherzinger E., Hasenbank R., Waelter S.,
Tait D., Colicelli J., Lehrach H.;
"HIP-I: a huntingtin interacting protein isolated by the yeast two-
                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 82-995 FROM N.A.
MEDLINE=97285121; PubMed=9140394;
Malchman M.A., Kolde H.B., McCutcheon K., Graham R.K., Nichol K.,
Nishlyama K., Kazemi-Esfariani P., Lynn F.C., Wellington C.,
Metzler M., Goldberg Y.P., Kanazawa I., Geitz R.D., Hayden M.R.;
"HIPl, a human homologue of S. cerevisiae Sla2p, interacts with
membrane-associated huntingtin in the brain.";
                                                                                                                                                                                                                                                                                              Hug A.H.M.M., Nichol K., Osborne L., Scherer S.W., Squitieri F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: THE AFFINITY OF THE HUNTINGTIN PROTEIN-HIP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 82-159 FROM N.A.
Bradshaw H., Hinds K., Harrison M.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Huntingtin interacting protein 1 (HIP-I) (Fragment).
               995 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE SLA2 FAMILY.
               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hybrid system.";
Hum. Mol. Genet. 6:487-495(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 203-602 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nat. Genet. 16:44-53(1997)
               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                 NCBI_TaxID=9606;
             HIP1_HUMAN
000291; 000328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NETWORKS.
                                                                                                                                                                                                                                                                                                                       Hayden M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IN BRAIN
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Gaps
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01-FEB-1995 (Rel. 31, Last sequence update)
01-GT-1996 (Rel. 34, Last annotation update)
Heat shock factor protein (HSF) (Heat shock transcription factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TALIN-LIKE.
KLHSCLP -> EFAAAST (IN REF. 4).
LNOLEE -> STRPRI (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72BDAA16AFD15C40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.0%; Score 55.5; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322 SONGVNKDEKDHLIERLYREISGLKAQLENMKT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SKSGKGKDDLRNEIDKLWREVNSLK-EMQALQT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog).
                                                             JOINED.
                                                                                                                                                                             JOINED.
                                                                                                                                                                                                      JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111633 MW;
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR001026; ENTH.
InterPro: IPR00258; ILWEQ.
Pfam; PF01417; ENTH; 1.
Pfam; PF01608; ILWEQ; 1.
ProDom; PF011820; ILWEQ; 1.
SMART; SM00373; ENTH; 1.
SMART; SM00307; ILWEQ; 1.
                                                                                                                                                                                                                                                                                                                                                U79734; AAC51257.1; -. AC004491; AAC08319.1;
                                                                                                                                                                                                                                                                                                                                                                        CAA70574.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:4913; HIP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              995 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 11; Conserv
                                                                                                                                                                                                                                                                                               AF052284;
                                                                                                                                                                                                                                                                                                                      AF052286;
                                                              AF052266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326
                                                  AF052265;
                                                                                                                                                                                                                                                                                                                                    AF052287;
                                                                                                                                                                                                                                                                                                                                                                          Y09420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSF1 OR HSF.
                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 601767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSF_XENLA
P41154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                       EMBL;
EMBL;
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EMBL;
EMBL;
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EMBL;
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EMBL;
EMBL;
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EMBL;
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EMBL;
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EMBL;
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EMBL;
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Matches
                                                                                                               EMBL;
                                                                                                                                                                                                                                                          EMBL;
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Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAFF_HUMAN
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      \mathbb{R}^{N}
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                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                        -1- FUNCTION: DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT SHOCK PROMOTER ELEMENTS (HSE) AND ACTIVATES TRANSCRIPTION (BY
                     MEDLINE-95369690; PubMed-7642097;
Stunp DG., Landsberger N., Wolffe A.P.;
"The CDNA encoding Nempus laevis heat-shock factor 1 (XHSF1):
nucleotide and deduced amino-acid sequences, and properties of the
                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00434; HSF_DOMAIN; 1.
Transcription regulation; Nuclear protein; DNA-binding; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transcription factor MafF (V-maf musculoaponeurotic fibrosarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Onodera K., Shavit J.A., Motohashi H., Katsuoka F., Akasaka J.-E. Engel J.D., Yamamoto M.; "Characterization of the murine maff gene."; J. Biol. Chem. 274:21162-21169(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Match 29.7%; Score 55; DB 1; Length 451; Local Similarity 34.2%; Pred. No. 12; les 13; Conservative 8; Mismatches 9; Indels
                                                                                                                         -!- SUBUNIT: HOMOTRIMER.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- PTM: EXHIBITS TEMPERATURE-DEPENDENT PHOSPHORYLATION (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE HSF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
; 3E271549BBCABB10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KSGKGKDD-----LRNEIDKLWREVNSLKEMQALQ 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
                                                                                                                                                                                                                                                                                                    PRINTS; PRO0056; HSFDOMAIN.
Probom; PD001788; HSF_DNA_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          451 AA; 49472 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphorylation; Heat shock.
                                                                                                                                                                                                                                                                                        EMBL; L36924; AAA99999.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                               Gene 160:207-211(1995).
                                                                                                                                                                                                                                                                                                                                                                                     SM00415; HSF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                   P22813; 1HKT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oncogene homolog F). MAFF.
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                   encoded protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed-10409670;
                                                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-129/SvJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAFF_MOUSE
054791;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAFF_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
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the extraembryonic and embryonic regions. At 8.5 dpc, weakly expressed in the future gut, allantois, yolk sace endoderm and the expressed in the future gut, allantois, yolk sace endoderm and the ectoplacental cone. At 9.5 dpc, strong expression in the primordial gut and presumptive fetal liver, in the floorplate of the myelencephalon, neural crest calls, sponglotrophoblasts, and giant cells of the placenta. At 12.5 dpc, detected in hepotocytes, in the outflow tract of the heart in a specific subset of dorsal root ganglia, in the cranial nerve ganglia, in the lung primordium, and in the epithelium of the expiratory tract. In newborn, strongly expressed in keratinocytes, in the cartilage, in bronchial epithelia, and bone membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
-i-FUNCTION: Interacts with the upstream promoter region of the oxytocin receptor gene. May be a transcriptional enhancer in the upstread at promoter region of the oxytocin receptor gene at parturition. Since upregulation of the oxytocin receptor gene at parturition. Since it lacks a putative transactivation domain, it may behave as a transcriptional repressor when it dimerize among himself. May also serve as a transcriptional activator by dimerizing with other (usually larger) basic-zipper proteins and recruiting them to specific DNA-binding sites. May be involved in the cellular stress
                                                                                                                                                                                                                                                                                                    SUBGUNIT: Monomer and homo- or heterodimer (By similarity).
SUBCELULIAR LOCATION: Nuclear (By similarity)
TISSUE SPECIFICITY: Highly expressed in the lung, lower expression
in the brain, thymus, liver, spleen, intestin, kidney, heart,
muscle, and ovary. Not significantly expressed in hematopoletic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcription regulation; DNA-binding; Repressor; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transcription factor Maff (V-maf musculoaponeurotic fibrosarcoma oncogene homolog F) (U-Maf).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86 114 LEUCINE-ZIPPER.
156 AA; 16954 MW; 574DD05499819037 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 4.3;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASIC MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 KGKDDLRNEIDKLWREVNSLK-EMQALQTVC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB009694; BAA24029.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC022952; AAH22952.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:96910; Maff.
InterPro; IPR004827; TF_bZIP.
InterPro; IPR004826; TF_Maf.
Pfam; PF03131; bZIP_Maf; 1.
SMART; SM00338; BRLZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.5%;
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Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
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                                                                                                                                                                                                                                                                               response.
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Q9ULX9; Q9Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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INDUCTION
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     δ
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RAMEDLINE-20057165; Pubbed-10591208;

RA Could A. R., Collins J.E., Bruskiewich R., Beare D.M., Colubman I., Hunt A.R., Collins J.E., Bruskiewich R., Beaseley O.P., Babagog A.K., Bagguley C., Balakey S.E., Bridgeman A.M.; Buck D., Burgess J., Ramalow K.P., Batcs K.N., Beaseley O.P., Burdy V.E., Colle C.G., Collier R.E., Connor R., Corby N.R., Colle C.G., Collier R.E., Connor R., Corby N.R., Corby N.R., Colle G.J., Cox A.V., Davis J., Dawson E., Raman P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Raman P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Raman P.D., Jones M.C., Kershaw J., Kinder A.M., Hols., Hall C., Kaller G.K., Carfann D.V., Griffths M.N.D., Hall C., Raman P.D., Jones M.C., Kershaw J., Kinder A.M., King A., Lard G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M., Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mcclaren S., McMurray A.A., Millie S.A., Mortlanor B.J.C., Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers I., Ross M.T., Shord C.D., Smalley S., Smith M.L., Scott C.E., Shra H.K., Stuce C.D., Smalley S., Smith M.L., Rodell C.N., Parlyn G.C., Spragon L., Steward C.A., Sulston J.E., Swann R.M., Wall M., Wallis S.M., Whilee I.W., Willey D.L., Wann R.M., Wall M., Wallis S.M., Whileeley M.N., Willey D.L., Wann R.M., Wall M., Wallis S.M., Whileeley M.N., Willey D.L., Wann R.M., Shibuya K., Yoshizaki Y., Aoki N., Willey D.L., Mann M., Shibuya K., Yoshizaki Y., Aoki N., Willey J., Miller N., Mann S., Qi, S., Lin S., P.P., Loh P., Malaj E., Nuyuen T., Pan H., Ruwis S., Lin S., Lin S., P., Loh, P., Walaj E., Nuyuen T., Pan H., Ruwis S., Lin S., Lin S., P., Loh P., Malaj E., Nuyuen T., Pan H., Ruwis S., Lin S., Lin S., P., Loh, W., Wann S., Qi, S., Baller N., Wann S., Qi, S., Qidan D., Song L., Rhas S., Radeh M., Duz S., Fulton L., Goela D., Graves T., Hawkins J., Harteille P., Wanng Y., Wanng Z., Wanne B., Earfeille P., Wanne S., Chissoe S., Murtay J., Wallers D., Wordes M., Du Z., Fulton L., Goela D., Gortes W., Wong Y., Wong Y., W
                                                                                           Kimura T., Ivell R., Rust W., Mizumoto Y., Ogita K., Kusui C., Matsumura Y., Azuma C., Murata Y.; "Molecular cloning of a human Maff homologue, which specifically binds to the oxytocin receptor gene in term myometrium."; Biochem. Biophys. Res. Commun. 264:86-92(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L., Kim U.J., Shitaya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,
                                                                                                                                                                                                                          Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Suishikawa T., Magai K., Sugano S., Ishibashi T., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y., Salto K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                           "NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 402:489-495(1999).
                                                                                                                                                                                                                                                                                          Masuho Y., Kanehori K.;
                                                                  TISSUE-Term myometrium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tilahun Y., Wright H.;
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                                                                                                                                                                                                            TISSUE-Placenta;
               NCBI_TaxID=9606;
                                                                               PubMed-10527846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Skin;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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the Buropean Bloinformatics Institute. There are no restrictions on its
use by non-profit institutions along as its content is in no way
modified and this statement is not removed. Usage by and for commercial
                                                                                                              Biochem. J. 361:371-377(2002).

-1- FUNCTION: Interacts with the upstream promoter region of the oxytocin receptor gene. May be a transcriptional enhancer in the upregulation of the oxytocin receptor gene at parturition. Since it lacks a putative transactivation domain, it may behave as a transcriptional repressor when it dimerize among himself. May also serve as a transcriptional activator by dimerizing with other (usually larger) basic-zipper proteins and recruiting them to specific DNA-binding sites. May be involved in the cellular stress
                                                                                                                                                                                                                                                                                                                                                                                                                     - Inspendent Monomer and homo- or heterodimer.
-- SUBBUNIT: Monomer and homo- or heterodimer.
-- SUBCELLULAR LOCATION: Nuclear.
-- INDUCTION: By oxidative stress.
-- TISSUE SPECIFICITY: Expressed in the term myometrium and kidney.
-- SIMILARITY: BELONGS TO THE B2IP FAMILY. MAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulation; DNA-binding; Repressor; Nuclear protein. 33 83 83 BASIC MOTIF. 36 114 LEUCINE-ZIPPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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01-0CT-1994 (Rel. 30, Last annotation update)
Hypothetical 14.2 kDa protein in RIM2-MSI1 intergenic region.
                         Moran J.A., Dahl E.L., Mulcahy R.T.;
"Differential induction of maff, mafG and mafK expression by
electrophile-response-element activators.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.5%; Score 54.5; DB 1; Length 164; 41.9%; Pred. No. 4.6; Live 7; Mismatches 10; Indels 1
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; FC34D9FF317E5EE1 CRC64;
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01-OCT-1994 (Rel. 30, Last sequ
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InterPro; IPR004826; TF_maf.
Pfam; PF03131; bZIP maf; 1.
SMART; SM00338; BRLZ; 1.
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PubMed-11772409;
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P38305;
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RT "RIM2, MSI1 and PGI1 are located within an 8 kb segment of Saccharomyces cerevisiae chromosome II, which also contains the Putative ribosomal gene L21 and a new putative essential gene with a reuchne alpher motif.";

Lucine 2 pper motif.";

Yeast 9:645-659(1993).

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DR EMBL; 224087; CAA79681.1; ---

DR EMBL; 236063; CAA8156.1; ---

DR FUR; S34019; S34019.

SGD: SGOUSD38; YBR194W.

W Hypothetical protein.

SQ SEQUENCE 123 AA; 14234 MW; AF25FE81D22D4C8C.CRC64;

Ouery Match

Best Local Similarity 44.4%; pred. No. 3.9;

Matches 12; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
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Search completed: April 15, 2003, 11:48:35 Job time: 7.5 secs

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077390 plasmodium
063717 rattus norv
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Maximum DB
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Q88til plasmodium
Q9v217 prococcus
Q9v27 prococcus
Q9v25 macaca fasc
Q9v25 macaca fasc
Q9v25 drosophila
Q0705 homo sapien
Q0705 homo sapien
Q91041 paralichthy
Q91041 paralichthy
Q91041 paralichthy
Q90471 drosophila
Q9005 rabbit fibr
Q9q05 staphylococ
Q85604 oryza sativ
Q9475 petunia int
Q9475 petunia int
Q9479 caenorhabdi
Q9rn31 bacillus an
Q9rn31 bacillus an
Q9rn31 bacillus an
Q9rn31 sulfolobus
Q9474 homo sapien
Q9474 caenorhabdi
Q9477 caenorhabdi
Q9477 caenorhabdi
Q9477 caenorhabdi
              Q9qus3 mus musculu O97594 bos taurus O57378 gallus gall Q8r3f2 mus musculu
060464 homo sapien
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ALIGNMENTS

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SEQUENCE FROM N.A.
STRAIN=ES129/SV;
Neame P.J., Grimm D.R.;
Mouse homolog of human CLECSF1, a cartilage derived C-type lectin.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF317204; AAG48620.1;
InterPro; IPR001304; Lectin.C.
Pfam; PF00059; lectin.c.
Pfam; PR00059; lectin.c.
PROSITE; PS00615; C-TYPE_LECTIN.1; 1.
PROSITE; PS00615; C-TYPE_LECTIN.1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
C-type lectin superfamily 1.

Mus musculus (Mouse)
Musmmalia; Mutazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Musmmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lectin.
SEQUENCE 196 AA; 22191 MW; 9AE4C809D119E852 CRC64;
196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 DDLRNEIDKLWREVNSLKEMQALQTVCLK 36
PRT;
PRELIMINARY;
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197 AA.

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PRELIMINARY;

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Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Perromyzontiformes; Petromyzontidae; Lampetra.
                                                                                                                                                                                                                                                                                                                        L SUBMITTED (JUN-2000) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
R EMBL; AJ40159; CAC24702.1; -.
R InterPro; IPR001664; IF.
R InterPro; IPR003657; Keratin_I.
R PITERP: PF00138; filament; 1.
R PRINTS; PR01248; TYPEIKERATIN.
R PRINTS; PR01248; TYPEIKERATIN.
R PRINTS; PR01276; TYPEZERRATIN.
R PRINTS; PR01276; TYPEZERRATIN.
R PROSITE; PS00226; IF; 1.
Colled Coil; Intermediate filament.
Q SEQUENCE 478 AA; 51130 MW; A7A16BDC57AB9D41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-81-176;
Lin J., Michel L.O., Zhang Q.;
Lin J., Michel L.O., zhang Q.;
"CmeABC functions as a multidrug efflux system in Campylobacter
jejuni.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF466820; AAL74245.1;
SEQUENCE 1040 AA: 113962 MW; BABD50F09F2B69BE CRC64;
                                                                                                                                                                                                                                                                     Schultess J., Schaffeld M., Markl J.;
"Type II keratin; intermediate filament protein from Lampetra
fluviatilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.1%; Score 65; DB 13; 45.7%; Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SKSGKGKDDL---RNEIDKLWREVNSLK-EMQALQ 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1040 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|||| |::::|| | || |:::|| 681 NKSGKSYDEIQKDVNKLVAAANQRKELSRVRT 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SKSGKGKDDLRNEIDKLWREVNSLKEMQALQT 32
                                                                                                                                                               Lampetra fluviatilis (River lamprey).
                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                       01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Conservative
                                    PRELIMINARY;
                                                                                                                              Keratin type II Lfl-K 1.
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                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                     NCBI_TaxID-7748;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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                                                                                                                                             KERATIN
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QBRTE4;
                                  Q98TQ7
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RESULT 4
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             Q98TQ7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                   01-NOV-1996 (TrEMBLrel. 01, Last Sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
C-type lectin homolog precursor.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 197;
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46.5%; Score 86; DB 13; Length 201;
Best Local Similarity 41.2%; Pred. No. 0.0053;
Matches 21; Conservative 7; Mismatches 7; Indels
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22 QNGKGRQRPAASKKDGVSLKMIEDLKAMIDNISQEVALLKEKQALQTVCLK 72
                                                                                                                                                                                                 TISSUE-CARTILAGE,
Neame P.J., Boynton R.E.;
"C-type lectin homolog from bovine cartilage.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; U22298; AAC18614.1;
HSSP; P05452; ITN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wewer, v.m.,
"tetranectin in chicken.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, A2277116; CAC20217.1; -
HSSP; P05452. 1TN3.
InterPro; IPR001304; Lectin_C.
Ffam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00015; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 201 AA; 22172 MM; 7C7F235D24426AEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 C-TYPE LECTIN HOMOLOG.
22215 MW; AAAC4280F41AC0F4 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 67.3%; Score 124.5; DB 6; Best Local Similarity 72.7%; Pred. No. 8.9e-08; Matches 24; Conservative 6; Mismatches 2;
                                                                                                                                                                                                                                                                                                              InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMARY; SM00034; CLECT; 1.
PR051TE; PS00615; C_IYPE_LECTIN_1; UNKNOWN_1.
PROSITE; PS50041; C_IYPE_LECTIN_2; 1.
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 01-NOV-1996 (TrEMBLrel. 01, Created)
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
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197
                                                                                                                               Bovidae; Bovinae; Bos.
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197 AA;
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                                                                                                                                                   NCBI_TaxID=9913;
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Indels

Length 478;

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Gaps

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C28E3A45B6201EF4 CRC64;

126205 MW;

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Plant Physiol. 126:1331-1340(2001).
EMBL; AF275345; AAK84476.1; -.
                           l protein.
1105 AA; 1
                           . Hypothetical
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Best Local Simi
Matches 11;
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                                                                                                            Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum (Tomato).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eparmatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Irish E.E., Wing R.A.;
"JOINTLESS is a MADS-box gene controlling tomato flower abscission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CV. HEINZ 1706; TRANSPOSON-FOLDBACK TRANSPOSON TAPIR1;
MEDLINE-20426111; Pubmed-10972295;
MAGO L., Begum D., Chuang H.W., Budiman M.A., Szymkowiak E.J.,
Irish E.E., Wing R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-CV. HEINZ 1706; TRANSPOSON-FOLDBACK TRANSPOSON TAPIR1;
MEDLINE-2131421; PubMed-11457984;
Mao L., Begum D., Goff S.A., Wing R.A.;
"Sequence and analysis of the tomato jointless locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.0%; Score 61; DB 16; Length 1040; 34.4%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
SEQUENCE 1040 AA, 113966 MW; 022005EDA20BE4C4 CRC64;
                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 126.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                          PRT; 1040 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SKSGKGKDDLRNEIDKLWREVNSLKEMQALQT 32
                                                                                                                                                                                                                                                                                                                                                    IPR000731; HMGCR/patch_5TM
                                                                                                                                                                                      STRAIN-NCTC 11168;
MEDLINE-20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K.,
                                                                                                                                                                                                                                                                                        reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                                                                                                                                                                                                EMBL; AL139075; CAB74202.1; -.
InterPro; IPR001036; Acrflvin_res.
InterPro; IPR004764; HAEL.
                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00702; ACRIFLAVINRP.
TIGRFAMS; TIGR00915; 2A0602; 1.
PROSITE; PS50156; SSp; 2.
                                                                                    ransmembrane efflux protein.
                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00873; ACR_tran; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 406:910-913(2000).
                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                  NCBI_TaxID=197;
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Best Local Simi
Matches 11;
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                                    09PID6;
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                        9dI460
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RESULT 6
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             90IGO
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PubMed-11572479;
Rawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
Sekine M., Baba S.-I., Ankal A., Kosuqi H., Hosoyama A., Fukui S.,
Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Rushida N., Oguchi A.,
Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
Oshima T., Kikuchi H.;
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
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     Length 1105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7."; DNN Res. 8:123-140(2001).
EMBL; AP000988; BAB57042.1; -
Hypothetical protein; Complete proteome.
SEQUENCE 324 AA; 37895 MW; 3E0F5C5876ED4244 CRC64;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
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Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBL_TaxID=63363;
                                                                                                                                                                                                                                                                                                               Q96284;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein ST1947.
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Elongation factor SELB.
SELB OR AQ_1033.
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       DB 10;
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                                                                                                                                                                                                                                                                                          324 AA
                               Pred. No. 53;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
       Score 60;
                                                                                                                                          ||| || :: ||| ||: 341 KSGLTKDEALEEIDKLQRDILSLQTVK 367
                                                                                                             2 KSGKGKDDLRNEIDKLWREVNSLKEMQ 28
                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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MEDLINE=98196666; PubMed=9537320;
       32.4%;
48.1%;
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213 EKLNNEIDKLRKEINDLKD 231
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Query Match
Best Local Similarity 48.1
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sulfolobus tokodaii.
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RT CCC CCC CCC DR SQ SQ

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PRELIMINARY;
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       NCBI_TaxID=9606;
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SEQUENCE
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Q63717
ID Q6371
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REQUENCE FROM N.A.

RA MEDLINE-21866394; PubMed-11889109;
RA MEDLINE-21866394; PubMed-11889109;
RA MEDAITAL V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Rathartacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.;

RA Forstein M., Kyrpides N., Overbeek R.;

RA Toucleatum strain ATCC 25586 ";

R. J. Bacteriol. 1841:2005-2018(2002).

REMBL, AE010570; AAL94778.1;

RM ATP-binding; Complete proteome.

SEQUENCE 233 AA: 26805 MW; D2D8AE692B2D356F CRC64;
"L MATURE 392:353-358(1998).
"I MATURE 392:353-358(1998).
"I MATURE 392:353-358(1998).
"I SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
"IN TABL: AROUGO19: LETU_D:
"IN INTERPRO. IPR0001525; ER_GTPDind.
"IN INTERPRO. IPR0005255; Small.GTP.
"IN INTERPRO. IPR0005255; Small.GTP.
"IN THERPRO. IPR0009; GTP_EFTU; I.
"IN Ffam: PF00144; GTP_EFTU; I.
"IN Ffam: PF03144; GTP_EFTU, I.
"IN TIGREAMS; TIGR00475; small.GTP:
"IN TIGREAMS; TIGR00475; small.GTP:
"IN TIGREAMS; TIGR00031; small.GTP:
"IN TIGR00009; small.GTP:
"IN TIGRO. TIGR00009; small.GTP:
"IN TIGR00009; small.GT
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Lipoprotein releasing system ATP-binding protein lolb.
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Bacteria; Fusobacteria; Fusobacterium.
NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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Pred. No.
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WUGSC:H_DJ0870F17.1.
HOmo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SGKGKDDLRNEIDKLWREVNSLKEMQALQ 31
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37.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sest Local Similarity
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Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
Mungall K., Murphy L., Oliver K., Quail M.A., Rafandream M.-A.,
Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
"The complete nucleotide sequence of chromosome 3 of Plasmodium
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Local Similarity 42.4%; Pred. No. 8.9;
Los 14; Conservative 6; Mismatches 12; Indels
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2003 (TrEMBLrel. 20, Last annotation update)
PFC0720W, MAL3P6.5.
Plasmodium falciparum (1solate 3D7).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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SEQUENCE FROM N.A.
Bauer C., Langston Y., Harrison M., Lennox S.;
"The sequence of Homo sapiens PAC clone RP5-870F17.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                       Waterston R.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AC004911; AAC33131.1; -.
InterPro; IPR000531; TonB_boxc.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
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103
103 AA: 11347 MW; EE712650E3109C76 CRC64;
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Nature 400:532-538(1999).
EMBL; 298551; CABILL46.2; -.
Hypothetical protein.
SEQUENCE 461 AA; 54677 MW; 6A33BEC7628758C5 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Heat shock transcription factor 1 (Fragment).
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Q9LA12;
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   RESULT 15
                  Q9LAI2
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            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                             STRAIN-SPRAGUE DAWLEY, TISSUE-LIVER, SWamynathan S.K., Revathi C.J., Srinivas U.K.; "Cloning and characterization of rat heat shock transcription factor
                                                                                                                                                                                                                                                                                                                                      Gaps
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STRAIN=1299V31; TISSUE-LIVER;
MEDLINE-99047622; PubMed-9829985;
MEDLINE-99047622; PubMed-992985;
MEDLINE-99047622; PubMed-982985;
Lang Y., Koushik S., Dai R., Mivechi N.F.;
"Structural organization and promoter analysis of murine heat shock transcription factor-1 gene.";
Lynascription factor-1 gene.";
Lynascription factor-1 gene.";
EMBL; AF059275; AAC80425.1;
HSSP; P22813; 1HKY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                          Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases EMBL; X83094; CAA58149.1; -. HSSP; P22813; 1HKT.
                                                                                                                                                                                                                                                                      448 AA; 48719 MW; CE615F42DBA759D8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Heat shock transcription factor 1 (Fragment).
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InterPro; IPR0000232; HSF_DNA_bind.
InterPro; IPR0002341; HSF_ETS.
Pfam; PF00447; HSF_DNA-bind; 1.
PRINTS; PR000056; HSFDOMAIN.
ProDom; PD001788; HSF_DNA_bind; 1.
SNART; SM00415; HSF; 1.
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                                                                                                                                                                                                InterPro; IPR000232; HSE_DNA_bind.
Plam; PF00447; HSE_DNA-bind; 1.
ProDom; PD001788; HSE_DNA_bind; 1.
SWART; SM00415; HSF; 11.
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Matches 13; Conserv
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Best Local Similarity
Matches 13; Conserv
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SEQUENCE FROM N.A.
                                                       NCBI_TaxID=10116;
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SEQUENCE
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                                                                                                                                                                          Bacillus sp..NEB-606.
Bacteria, Firmlcutes; Bacillus/Clostridium group; Bacillales;
Bacillaceae; Bacillus.
NCBI_TaxID=114630;
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                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=NEW ENGLAD BIOLAB #606;
MEDLINE=2015577: PubMed=10646519;
Hsieh P.C., Xiao J.P., O'loane D., Xu S.Y.;
"Cloning, Expression, and Purification of a Thermostable Nonhomodimeric Restriction Enzyme, Bsll.";
J. Bacteriol. 182:949-955(2000).
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InterPro; IPR001091; CN4_Metransf.
InterPro; IPR00295; D21N6_mtfrase.
InterPro; IPR002941; N6/N4_Mtase.
Pfam; PF01555; N6_N4_Mtase.
PRINTS; PR00506; D21N6MTFRASE.
PRINTS; PR00508; S21NAMTFRASE.
PROSITE; PS00093; N4_MTASE; UNKNOWN_1.
SEQUENCE 912 AA; 107438 MW; BFFF7FIF86102C25 CRC64;
                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Pred. No. 1e+02;
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PRT;
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Best Local Similarity 37.9%;
Matches 11; Conservative
PRELIMINARY;
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Sequence 4,
Sequence 7,
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Patent No. 5739281
GENERAL INFORMATION:
APPLICANT: Thoegersen, Hans Christian
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of
TITLE OF INVENTION: proteins
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 960; DB 1; Pred. No. 2.4e-102;
                                     US-08-401-530A-4
US-08-822-54
US-08-822-562-4
US-08-802-562-6
US-08-401-530A-6
US-08-709-662-6
US-08-729-103-7
US-08-729-103-7
US-08-535-521-14
US-09-535-521-14
US-09-535-521-14
US-09-535-521-14
US-09-535-521-14
US-08-822-261-4
US-08-422-166-7
US-08-422-166-7
US-08-422-166-7
US-08-422-166-7
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                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: FEBRUARY 4, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 8906
TELEFAX: 617 542 8906
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STATE: Massachusetts
COUNTRY: USA
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Sequence 7, Appli
Sequence 4, Appli
Patent No. 5180808
Patent No. 5514582
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Patent No. 5514582
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Sequence 56,
Sequence 99,
Sequence 49,
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Sequence 6,
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(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-304-428B-49
US-09-118-602C-2
US-09-011-735-6
US-09-011-735-1
US-09-0129-156-1
PCT-US95-03747-2
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US-08-469-658-56
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                                                                                                                                                                                                                                                                                                                                                                               262574 seqs, 29422922 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                    protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5514582-17
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length DB
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125
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208
292
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174
1487
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Score

Result Š. 422.5 186.5 185.5 178.5 178.5

140.5 140.5 140.5 140.5

sed

Minimum DB Maximum DB

Database

Title: Perfect score:

Sequence:

protein

Run on:

Scoring table:

Searched:

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61 FLAFTQTKTFHEASEDCISRGGTLSTPQTGSENDALYEYLRQSVGNEAEIWLGLNDMAAE 120
                                                                                       GTWVDMTGARIAYKNWETEITAQPDGGKTENCAVLSGAANGKWFDKRCRDQLPYICQFGI 180
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 STPQTGSENDALYEYLRQSVGNEAEIWLGLNDMAAEGTWVDMTGARIAYKNWETEITAQP 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 ELKSRLDTLAQEVALLKEQQALQTVCLKGTKVHMKCFLAFTQTKTFHEASEDCISRGGTL 84
                                                                                                                                                      Sequence 49, Application US/08340428B
Patent No. 5648465
RENERAL INFORMATION:
APPLICANT: RAUCH, Use
APPLICANT: RAUCH, Use
TITLE OF INVENTION: CLONING, EXPRESSION AND USES FOR A
TITLE OF INVENTION: NEUROCAN AS A CHONDROITIN SULFATE PROTEOGLYCAN
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 197;
                                                                                                                                                                                                                                                                                                                     Sequence 99, Application US/09602877A
Patent No. 6422707
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: AU, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILLE REPERBENCE: 21011.44665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

Best Local Similarity 51.3%; Pred. No. 1.3e-40;
Matches 80; Conservative 27; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 DGGKTENCAVLSGAANGKWFDKRCRDQLPYICQFGI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/602,877A
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSEQ for Windows Version 3:0
SEQ ID NO 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Browdy and Neimark
419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapien
US-09-602-877A-99
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STREET: 41
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COUNTRY:
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                                                                                                61 FLAFTQTKTFHEASEDCISRGGTLSTPQTGSENDALYEYLRQSVGNEAEIWLGLNDMAAE 120
                                                                                                                  121 GTWVDMTGARIAVKNWETEITAQPDGGKTENCAVLSGAANGKWFDKRCRDQLPYICOFGI 180
              Gaps
                                                                                                                                                                                    EPPTOKPKKIVNAKKDVVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLKGTKVHMKC 60
                                                  22 EPPTOKPRKIVNAKKDVVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLKGTKVHMKC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPPTQKPKKIVNAKKDVVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLKGTKVHMKC 60
                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Th egersen, Hans Christian
APPLICANT: Holtet, Thor Las
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 202;
          0; Indels
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Pred. No. 2.4e-102;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
SOFTWARE: PATENTIN Release #1.0, Version
SOFTWARE: Ja.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
       Mismatches
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225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                      Sequence 56, Application US/08469658
Patent No. 5917018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
ATORNEY/AGENT INFORMATION:
NAME: PRUI T. Clark
REGISTRATION NUMBER: 30,162
REFREENCE/DOCKET NUMBER: 0636:
TELECHMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
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100.0%;
181; Conservative
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
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Best Local Similarity 100.0
Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: Massachusetts
COUNTRY: USA
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STREET: 22
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COMPUTER READABLE FORM

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APPLICANT: Wakamiya, No. 6110708utaka
TITLE OF INVENTION: Recombinant Conglutinin and Producing Method Thereof
FILE REFERENCE: 19036/34548
CURRENT APPLICATION NUMBER: US/09/011,735B
CURRENT FILING DATE: 1998-05-22
EARLIER APPLICATION NUMBER: UP 7-209698
EARLIER PILING DATE: 1995-08-17
NUMBER OF SEQ ID NOS: 1955-08-17
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09011735B
Patent No. 6110708
GENERAL INFORMATION:
APPLICANT: Wakamiya, No. 6110708utaka
TITLE OF INVENTION: Recombinant Conglutinin and Producing Method Thereof
FILE REFERENCE: 19036/34548
CURRENT APPLICATION NUMBER: US/09/011,735B
111 ERKALQTEMARIKKWLTFSLGKQVGNKFFLTNGEIMTFEKVKALCVKFQASVATPRNAAE 170
                                                                      53 GTKVHMKCFLAFTQTKTFHEASEDCISRGGTLSTPQTGSENDALYEYLRQSVGNEAEIWL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 GLNDMAAEGTWVDMTGARIAYKNWETEITAQPDGGKTENCAVLSGAANGKWFDKRCRDQL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHID STEGRETYPTGEILVYSNWADGEPUNSDEGQPENCVEI -- FFDGKWNDVPCSKQL 155
                                            93 NDALYEYLRQSVGNEAEIWLGLNDMAAEGTWVDMTGARIAYKNWETEITAQP-DGGKTEN 151
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; LOCATION: (6)
; OTHER INFORMATION: Xaa is a protein-constituting amino acid
US-09-011-735-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa is a protein-constituting amino acid
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                                                                                                                                    152 CAVLSGAANGKWFDKRCRDQLPYICQFGI 180
                                                                                                                                                                                222 CVLL--LKNGQWNDVPCSTSHLAVCEFPI 248
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; Sequence 6, Application US/09011735B

; Patent No. G110708

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Bovine
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TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC
TITLE OF INVENTION: YEAST
FILE REFERENCE: A7290
CURRENT APPLICATION UNMBER: US/09/198,603C
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1077 -NSFGHE-NSWIGLNDRTVERDFOWTDNTG--LQYENWREK---QPDNFFAGG--EDCVV 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VCLKGT-----KVHMKCFLAFTQTKTFHEASEDCISRGGTLSTPQTGSENDALYEYL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 RQSVGNEAEIWLGLNDMAAEG--TWVDMTGARIAYKNWETEITAQPD----GGKTENCAV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 14 NO. 5648465ember 1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5;
3e-12;
52;
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Thes 55;
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19.3%; Score 185.5;
Best Local Similarity 30.2%; Pred. No. 3.3e
Matches 45; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ed. No. 3e-1
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.4%; Score 186.5; 32.7%; Pred. No. 3e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSGAANGKWFDKRCRDQLPYICQFGIV 181
                                                                                                                                                    CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/922,911
FILING DATE: 03 August 1992
FILING TATE 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09198603C Patent No. 6337193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: TULLY, Raymond E. APPLICANT: CALTAGIRONE, G. Thomas APPLICANT: MOYER, Shawn S. APPLICANT: RONNIM?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                           NAME: Browdy, Roger L. REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: MAITELECOMMUNICATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1257 amino acids
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                     202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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nes 48; Conserv
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US-09-198-603C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-340-428B-49
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LENGTH: 248
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-029-156-1
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Diego
STATE: California
                                                                                    Query Match
Best Local Similarity
Matches 40; Conserv
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PCT-US95-03747-2
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                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                  Length 351;
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TITLE OF INVENTION: RECOMBINANT CONGLUTININ AND PRODUCING
TITLE OF INVENTION: METHOD THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
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APPLICATION NUMBER: US/09/029,156
                                                                                                                                                                                                                  DB 3;
                                                                                                                                                                                                          Query Match
18.6%; Score 178.5; DB 3
Best Local Similarity 31.7%; Pred. No. 3.6e-12;
Matches 40; Conservative 23; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
APPLICATION NUMBER: PCT/JP95/02035
FILING DATE: 02-0CT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JPA - 209698
FILING DATE: 17-AUG-1995
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19036/34546
CURRENT FILING DATE: 1998-05-22
EARLIER APPLICATION NUMBER: JP 7-209698
EARLIER FILING DATE: 1995-08-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/JP96/00173
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COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6365342
GENERAL INFORMATION:
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REGISTRATION NUMBER: 38,153
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TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 351 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
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                                                                                                                LENGTH: 351
TYPE: PRT
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                                                                                            SEQ ID NO 1
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                                                                                                            288 SMNDISTEGRETYPTGEILVYSNWADGEPNNSDEGOPENCVEI--FPDGKWNDVPCSKOL 345
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    Length 351;
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application PC/TUS9503747
GENERAL INFORMATION:
APPLICARY: LA JOLLA CANCER RESEARCH FOUNDATION
TITLE OF INVENTION: Brevican, A Glial Cell Proteoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03747
FILING DATE: 27-MAR-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPDGG--KTENCAVLSGAANGKWFDKRCRDQLPYICQFGIV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Campbell and Flores 4370 La Jolla Village Drive, Suite 700
  DB 4;
; Score 178.5; DB 4;
; Pred. No. 3.6e-12;
23; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 177; DB 5;
Pred. No. 2.3e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Imbra, Richard J.
REGISTRATION NUMBER: 37,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: FI
18.6%;
ilarity 31.7%;
Conservative 2
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TELEFAX: (619) 535-8049
INFORMATION FOR SEO ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 912 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 27.3%
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17.3%; Scc. 27.2%; Pred. No. /...
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                                       3: Zarley, McKee, Thomte,
801 Grand Ave. Suite 3200
                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION TELEPHONE: (515) 288-3667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (515) 288-1338
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: amino acids
                                                                                                                               STATE: Iowa
COUNTRY: United States
ZIP: 50309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-365-103B-6
                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
       CORRESPONDENCE ADDRESS:
                                                                                                          Des Moines
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Best Local Similarity
Matches 49; Conserv
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                                                                                                                                                                                                                                                                   APPLICANT: Lynch, Richard G
APPLICANT: Nunez, Raphael D.
APPLICANT: Yodol, Jungi
TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23
TITLE OF INVENTION: and Methods of Use for Same
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 IVNAKKDVVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLKGTKVHM----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Voorhees & Sease
774 QPDSYFLSGENCVVMVWHDQGQWSDVPCNYHLSYTCKMGLV 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,103B
FILING DATE: 28-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08365103B
Patent No. 576643
GENERAL INFORMATION
APPLICANT: Lynch, Richard G
APPLICANT: Nunez, Raphael D.
APPLICANT: Yodoi, Jungi
TITLE OF INVENTION: DNA Sequences for Soluble F)
TITLE OF INVENTION: and Methods of Use for Same NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 166; DB 1;
Pred. No. 7.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thomte,
STREET: 801 Grand Ave. Suite 3200
CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                      Sequence 4, Application US/08365103B Patent No. 5766943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37,719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.3%;
27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (515) 288-3667
TELEFAX: (515) 288-1388
INPORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 27.2*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 287 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Iowa
COUNTRY: United States
ZIP: 50309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-365-103B-4
                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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116 LVNIKSLGLNEK--RTASDSLEKLQEEVAKL----WIEILISKGTACNICPKNWLHFOOK 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 EGTWVDMTGARIAYKNWETEITAQP-DGGKTENCAVLSGAANGKWFDKRCRDQL-PYICQ 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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APPLICANT: Lynch, Richard G
APPLICANT: Nunez, Raphael D.
APPLICANT: Vodoi, Jungi
TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23
TITLE OF INVENTION: and Methods of Use for Same
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
STREET: 801 Grand Ave. Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 IVNAKKDVVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLKGTKVHM~
Voorhees & Sease
                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,103B
FILLIG DATE: 28-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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Pred. No. 7.7e-11;
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Query Match
Best Local Similarity
Matches 35; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
STREET: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-401-530A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 CYYFGKGSKQWIQARFACSDLQGRLVSIHSQKEQDFLWQHI-----NKKDSWIGLQDLNM 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 EGTWVDMTGARIAYKNWETEITAQP-DGGKTENCAVLSGAANGKWFDKRCRDQL-FYICQ 177
                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                               10 IVNAKKDVVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLKGTKVHM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                     Score 166; DB; Pred. No. 8.8e 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LASKY, LAURENCE A.
APPLICANT: WW, KAI
TITLE OF INVENTION: TYPE C LECTINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEE: Genentech, Inc.
1 460 Polht San Bruno Blvd
South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P1019R1
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Patent No. 6117977
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                                REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: U11
TELECOMMUNICATION INFORMATION:
                                                                                                                TELEPHONE: (515) 288-3667 TELEFAX: (515) 288-1338 INFORMATION FOR SEC ID NO: 2: SEQUENCE CHARACTERISTICS:
FILING DATE: 28-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                    327 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARCTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1479 amino acids
                                                                                                                                                                                                                                                                                                Best Local Similarity 27.28
Matches 49; Conservative
                                                  Nebel, Heidi S.
                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-365-1038-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-840-062-4
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US-08-840-062-4
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64 FTQTKTFHEASEDCISRGGTLSTPQTGSENDALYEYLRQSVGNEAEIWLGLNDMAAEGTW 123
                                                                                                                             253 FOSTLSWREAWASCEQOGADLLSITEIHEQIYINGLL---TGYSSTLWIGLNDLDTSGGW 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 FQSTLSWREAWASCEQQGADLLSITEIHEQTYINGLL--TGYSSTLWIGLNDLDTSGGW 308"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 FTQTKTFHEASEDÇISRGGTLSTPQTGSENDALYEYLRQSVGNEAEIWLGLNDMAAEGTW 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Gaps
                                                                                                                                                                           124 VDMTGARIAYKNWETEITAQPDGGKTENCAVLSGAANGKWFDKRCRDQLPYICQ 177
                                                                                                                                                                                                             310 QWSDNSPLKYLNWESD---QPDNPSEENCGVIRTESSGGWQNRDCSIALPRYCK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 QWSDNSPLKYLNWESD---QPDNPGEENCGVIRTESSGGWQNHDCSIALPYVCK 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 VDMTGARIAYKNWETEITAQPDGGKTENCAVLSGAANGKWFDKRCRDQLPYICQ 177
17.2%; Score 165; DB 3; Length 1479; 30.7%; Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                            20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.7%; Score 160; DB
30.7%; Pred. No. 4.3e-
tive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LASKY, LAURENCE A.
APPLICANT: WW, KAI
TITLE OF INVENTION: TYPE C LECTINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/840,062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSEE: Genentech, Inc.
f: 460 Point San Bruno Blvd
South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P1019R1
                                                                                                                                                                                                                                                                                            RESULT 14
US-008-840-062-2
'Sequence 2, Application US/08840062
'Patent No. 6117977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WinPatin (Genentech)
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Patent No. 5834590
GENERAL INFORMATION:
APPLICANT: Vinik, Aaron I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 30.74
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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70 FHEASEDCISR-GGTLSTPOTGSENDALYEYLROSVGNEAEIWLGLNDMAA-----EGTW 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 VDMTGARIAYKNWETEITAQPDGGKTENCAVLSGAANG-KWFDKRCRDQLPYICQF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
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1.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75; Indels
APPLICANT: Duquid, William P.
TITLE OF INVENTION: INGAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                       CUTY: n.c.
STATE: D.C.
COUNTRY: US
2 IP: 200014597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEATEN PC COMPATIBLE
COMPUTER: PATENT PC-DOS/MS-DOS
COFFATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-FEB-1995
CTELING DATE: 22-FEB-1995
TTELING DATE: 22-FEB-1995
TTELING DATE: APPLICATION:
APPLICATION: 800
TTELING DATE: APPLICATION:
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Best Local Similarity 26.7%; Pred. No. 1.4e
Matches 47; Conservative 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 22-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT, SATAH
NAME: KAGAN, SATAH A.
REGISTRATION NUMBER: 32, 141
REFERENCE/DOCKET NUMBER: 00570.48743
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                     SSEE: Banner & Allegretti
T: 1001 G Street, N.W.
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 174 amino acids; TYPE: amino acid
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Rattus rattus
US-08-401-530A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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The invention relates to polynucleotides encoding breast tumour polypeptides. The sequences are useful for treating cancer, preferably breast cancer, in a patient or for stimulating an immune response. The polynucleotides and polypeptides are also useful in the diagnosis and monitoring of breast cancer. A method for detecting the presence of a cancer in a patient, comprises obtaining a biological sample from the patient, contacting the biological sample with a binding agent that binds to a breast tumour polypeptide, detecting in the sample an amount of polypeptide that binds to the binding agent, and comparing the amount of polypeptide to a predetermined cut-off value, therefore determining the presence of a cancer in the patient. Sequences AAU82641-AAU82655 represent human breast tumour polypeptides of the invention.
                                                                   The present sequence is encoded by a cDNA sequence which was isolated from a breast tumour cDNA library. It is provided in a specification relating to compounds for immunotherapy and diagnosis of breast cancer. Breast tumour antigens and the polynucleotides that encode them may be used in the production of a pharmaceutical composition to be used in the treatment of breast cancer. Proliferated T cells and incubated antigen presenting cells are also required. The polypeptides and polynucleotides may also be used to produce a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotides encoding breast tumour polypeptides, useful for treating breast cancer or stimulating an immune response -
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86.1%; Pred. No. 5.8e-14;
ive 4; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                      Human breast tumour polypeptide clone #2.
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                                    Claim 2; Page 90-91; 95pp; English.
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12-OCT-2000; 2000US-0687507.
06-FEB-2001; 2001US-0778381.
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N-PSDB; ABK28980, ABK29015.
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Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
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                      Score 166; DB 23;
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4; Mismatches 1
                                                 1 RRVKEKDGDLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                           AAY66756 standard; protein; 206 AA
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                    90.7%;
illarity 86.1%;
Conservative
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11-AUG-1998
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The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors. TIE ligands and various enzymes. The membrane-bound proteins and receptor immunoadhesins, for instance, can be used as therapeutic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially
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86.1%; Pred. No. 6.1e-14;
tive 4; Mismatches
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Yuan J;
                                                             98US-0096960.
98US-0097022.
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N-PSDB; AAZ65102.
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and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammallan subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
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                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB65279
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dog: cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gurney AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Goddard A, Godowski PJ,
Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P, Chen J, Desnoyers L,
Smith V, Watanabe CK, W
                                                                                                                                                                                                                                                                                                            06-MAR-2000; 2000US-186968P-14-MAR-2000; 2000US-186968P-14-MAR-2000; 2000US-189320P-14-MAR-2000; 2000US-189320P-15-MAR-2000; 2000US-199320P-15-MAR-2000; 2000US-191007P-21-MAR-2000; 2000US-191007P-21-MAR-2000; 2000US-19114P-28-MAR-2000; 2000US-191314P-29-MAR-2000; 2000US-193053P-29-MAR-2000; 2000US-19449P-04-APR-2000; 2000US-194449P-04-APR-2000; 2000US-194449P-04-APR-2000; 2000US-194647P-11-APR-2000; 2000US-19669D-11-APR-2000; 2000US-19669D-11-APR-2000; 2000US-19669D-11-APR-2000; 2000US-19669D-11-APR-2000; 2000US-19669D-11-APR-2000; 2000US-19669D-11-APR-2000; 2000US-19668D-25-APR-2000; 2000US-199550P-25-APR-2000; 2000US-199550P-25-APR-2000; 2000US-199550P-25-APR-2000; 2000US-199550P-25-APR-2000; 2000US-199550P-25-APR-2000; 2000US-199550P-25-APR-2000; 2000US-199550P-25-APR-2000; 2000US-199530P-25-APR-2000; 2000US-199530P-25-APR-2000; 2000US-199530P-25-APR-2000; 2000US-199530P-25-APR-2000; 2000US-199530P-25-APR-2000; 2000US-199530P-25-APR-2000; 2000US-199530P-25-APR-2000; 2000US-199530P-25-APR-2000; 2000US-201516P-25-APR-2000; 2000US-201514041.
                                                                                                                                                                                                                   2001WO-US06520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-AUG-2000; 2000WO-US23328
08-NOV-2000; 2000WO-US30952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                               WO200168848-A2,
                                                                                          Homo sapiens.
                                                                                                                                                                                                           28-FEB-2001;
                                                                                                                                                                       20-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan J,
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(first entry)

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₽J;
                                                        Human; secreted and transmembrane protein; PRO; cytostatic;
cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
diagnostic assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Botstein D, Desnoyers L, Eaton DL;
er H, Gerritsen ME, Goddard A, Godowski
Kljavin IJ, Napier MA, Pan J, Paonl NF;
                                                                                                                                                                                 99US-0141037.
99US-0143048.
99US-0144758.
99US-0145698.
                                                                                                                                                                                                                                                                                               20-DEC-1999; 99WO-US30911.
05-JAN-2000; 2000WO-US00219
06-JAN-2000; 2000WO-US00376.
11-FEB-2000; 2000WO-US03355.
18-FEB-2000; 2000WO-US04341.
                                                                                                                                                      2000WO-US08439
                                                                                                                                                                                                                     99US-0146222
99US-0149396
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99WO-US21547
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                                                                                                                                                                                                                                                                                                                                                                                                                               Ashkenazi AJ, Baker KP, Bo
Ferrara N, Fong S, Gerber
Grimaldi CJ, Gurney AL, Kl
                                                                                                                                                                                                                                                                              99WO-US28301
                                                                                                                                                                                                                                                                                                                                                      2000WO-US04914
2000WO-US05004
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Fong S, Gerbe
J, Gurney AL,
                                                                                                               WO200073454-A1.
                                                                                              Homo sapiens
                                                                                                                                                      30-MAR-2000;
                                                                                                                                                                                23.JUN-1999
07-JUL-1999
26.JUL-1999
17.AUG-1999
115.SEP-1999
115.SEP-1999
115.SEP-1999
30.NOV-1999
30.NOV-1999
11.EEC-1999
11.EEC-1999
11.EEC-1999
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22-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                       24-FEB-2000;
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                                                                                                                                   07-DEC-2000
                                                                                                                                                                        02-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                          20-MAR-2000;
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Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats

Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -

WPI; 2001-602746/68. N-PSDB; AAS46062.

Claim 11; Fig 276; 774pp; English.

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97DK-0000685
              23-AUG-2001; 2001WO-US26626
                                                                                                                                                                                            N-PSDB; AAD32720.
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                                                                                                                                               Ashkenazi AJ,
Williams PM,
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                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW94264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                               The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bloactive molecules, such as conclusive and their standard send that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays.

ARF4270 to AAF4470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AF44087 to AAF4269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein can be exemplification of the present invention.
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0
                                                                                                                                                                                                                                                                                                                                                     Gaps
  Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; tumour-associated antigenic target-173; TAT173; cytostatic; gene therapy; tumour; breast; lung; liver; stomach; cancer; ADEPT; antibody-dependent enzyme mediated prodrug therapy.
                                                                PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death -
                                                                                                                                                                                                                                                                                                                                                    ;
0
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                                                                                                                                                                                                                                                                                                                                Length 206;
Tumas D, Watanabe CK, Williams PM,
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "C-type lectin domain signature"
                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                            / Match 90.7%; Score 166; DB 22; Local Similarity 86.1%; Pred. No. 6.1e-14; nes 31; Conservative 4; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32..206
/label= Mature_TAT173_protein
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/label= N-myristoylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155..161
/label= N-myristoylation_site
                                                                                                                                                                                                                                                                                                                                                                        1.31
/label- Signal_peptide
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/label- Amidation_site
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/label= Amidation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE20465 standard; Protein; 206 AA.
                                                                                                             Claim 12; Fig 288; 935pp; English.
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  Stewart TA,
                                WPI; 2001-032160/04.
                                            N-PSDB; AAF44248
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Active-site
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                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE20465;
           Zhang Z;
                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
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The present invention relates to an isolated antibody that binds to tumor-associated antigenic target (TAT) polypeptide. The antibody is used for treating and diagnosing tumours (e.g. breast, lung, liver or stomach tumours) in mammals, e.g. dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, or preferably humans. The antibody may also be used in antibody-dependent enzyme mediated prodrug therapy (ADEPT). The antibody is also useful for the therapeutic treatment or for the diagnostic detection of cancer. TAT cDNA is useful in gene therapy. The present sequence is human TAT173 protein. TAT173 cDNA is designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; H6FXTN23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides, useful for treating and diagnosing tumor (e.g. breast, lung, liver or stomach tumor) in mammals, e.g. dogs, cats, cattle, pigs, goats, rabbits or humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antibodies that bind tumor-associated antigenic target (TAT)
                                                                                                                                                                                                                                                                                                                                                              Gurney AL, Polakis P;
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86.1%; Pred. No. 6.1e-14;
ive 4; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 10; 124pp; English.
24-AUG-2000; 2000WO-US23328.
01-DEC-2000; 2000WO-US32678.
28-FEB-2001; 2001WO-US06520.
                                                                                                    01.JUN-2001; 2001MO-US17800
20-JUN-2001; 2001MO-US19692.
29-JUN-2001; 2001MO-US21066.
09-JUL-2001; 2001MO-US21735.
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                                                                                                                                                                                                                                                                                                                                                                                            Wood WI,
                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
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Best Local Similarity
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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranecth protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural construct comprise at least one tetranectin trimerising structural construct comprise at least one tetranectin trimerising structural construct compares with a large scale of forming a stable complex with 2 other construct on proteins CIHGFXTN123, H6FXTN123, H6FXTN13, H6FX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                     New monomer polypeptide constructs for diagnosis and therapy - comprise a tetranectin trimerising structural element covalently linked to at least one heterologous molety for providing functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;. Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.2%; Score 79; DB 20; Length 180; 57.1%; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                    Kastrup JS;
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                                                                                                                                               JH, Holtet TL,
Thogersen HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 8; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW94256 standard; protein; 181 AA.
                                                                                                                                            Graversen NJH,
                     (ETZE/) ETZERODT M.
(GRAV/) GRAVERSEN N J H.
(HOLT/) HOLTET T L.
(KAST/) KASTRUP J S.
                                                                                                                                                                Nielsen BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                         WPI; 1999-080897/07.
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                                                                                                                                        Etzerodt M,
                                                                                                                                                                Larsen IK,
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16;
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New monomer polypeptide constructs for diagnosis and therapy - comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional

Claim 10; Page 60; 110pp; English.

activity

Kastrup JS;

JH, Holtet TL, Thogersen HC;

NJH,

Graversen

Etzerodt M,

GRAVERSEN N J

ETZERODT M.

(ETZE/) 1 (GRAV/) (

(HOLT/) HOLTET T L. (KAST/) KASTRUP J S.

HOLTET T

HOLT

Larsen IK, Nielsen BB,

WPI; 1999-080897/07

98WO-DK00245. 97DK-0000685.

11-JUN-1998; 11-JUN-1997;

.7-DEC-1998

Homo sapiens. WO9856906-A1.

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The invention relates to the design of trimeric polypeptides using collypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural construct comprise at least one tetranectin trimerising structural molecy, the TYSE being capable of forming a stable complex with 2 other molecy, the TYSE being capable of forming a stable complex with 2 other any of the fusion proteins CITHGFXNN123, H6FXTN123, H6FXTN123, H6FXTN123, CAMM94261 to AMM94264). The TYSE can be used for the construction of structure, a toxin, a detectable label, an in situ activatable substance, a nadioactive molety, a cytokine, a non-proteinaceous polymer, or a protein can be used as vehicles of for assembling antibody fragments into oligomeric or multivalent construct to a target. They can be used as vehicles of the structures can be used as vehicles of preselected pharmaconshiner; and for targeted agency phacing selective constructs. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific population of cells. They can also be used for delivering a substance of acill or tissue or for delivering an imaging or toxin-conjugated antibody to a tumour. They can also be used for prevention or treating a disease or for diagnosis. The TTSE provides a stable structure which can act as a vehicle for a wide variety of conjugates. The present sequence represents a human tetranectin sequence from which the TTSE can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.01
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 DLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW94262 standard; protein; 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW94262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW94262
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Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin

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Human tetranectin amino acid seguence.

26-APR-1999 (first entry)

AAW94256;

à Dρ 7

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AAR60521 standard; Protein; 202 AA.
                                                                                                                                                                                  22-MAR-1995 (first entry)
                                                                                                                                                                                                                                       Human tetranectin.
                                                                                                                                AAR60521;
                               RESULT 10
                                                       AAR6052
                                                                                                         δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural element (TFSE) which is covalently linked to at least one heterologous moiety, the TTSE being capable of forming a stable complex with 2 other TTSE, with the proviso that the heterologous moiety is different from any of the fusion proteins CIH6FXTN123, H6FXTN123, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                               Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; HGFXTM123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New monomer polypeptide constructs for diagnosis and therapy - comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holtet TL, Kastrup JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thogersen HC;
H6FXTN123 fusion protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Fig 6; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Graversen NJH,
                                                                                                                                                                                                                                                                                                                                98WO-DK00245
                                                                                                                                                                                                                                                                                                                                                                                  97DK-0000685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRAVERSEN N J H. HOLTET T L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nielsen BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GRAV/) GRAVERSEN N
(HOLT/) HOLTET T L.
(KAST/) KASTRUP J S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-080897/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    (ETZE/) ETZERODT M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 AA;
                                                                                                                                                                                                                                                                                                                                                                                  11-JUN-1997;
                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                11-JUN-1998;
                                                                                                                                                                                                                                                                                    17-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Etzerodt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Larsen IK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sednence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
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cDNA encoding human tetranectin (full sequence given in AAR60521) was PCR amplified using primers given in AAQ71274-75. Amplified cDNA was linked to a sequence encoding the Factor-Xa cleavage site (given in AAR60503), subcloned in vector p77H6 so that it was linked to a hexahistidine-encoding sequence and expressed in E. coli BL21. The fusion protein was purified on an Ni2+-activated NTA-agarose column. A cyclic procedure was used to obtain correctly folded recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Refolding of polypeptide molecules - using a cyclic process involving denaturing and renaturing conditions to produce a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.2%; Score 79; DB 15; Length 202; 57.1%; Pred. No. 0.016; ive 7; Mismatches 5; Indels
Serine protease; Factor-Xa; recognition site; tetranectin; fusion protein cleavage; protein folding; primer; polymerase chain reaction; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human EST encoded protein SEQ ID NO: 1559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 151-52; 202pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Etzerodt M, Holtet TL, Thogersen HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 DLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ā
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                                                                                                                                                                                                                                                                                  93DK-0000130.
93DK-0000139.
93WO-GB02492.
                                                                                                                                                                                                                                       94WO-DK00054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     involving denaturing a correctly folded prod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-279681/34.
                                                                                                                                                                                                                                                                                                                                                                                     (DENZ-) DENZYME APS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 AA;
                                                                                              Homo sapiens
                                                                                                                                                                                                                                       04-FEB-1994;
                                                                                                                                                                                                                                                                                       04-FEB-1993;
                                                                                                                                                                                                                                                                                                               05-FEB-1993;
03-DEC-1993;
                                                                                                                                              WO9418227-A.
                                                                                                                                                                                             18-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM24034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
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DLKTQVEKLWREVNALKEMQALQTVCLR 36 41 ELKSRLDTLAQEVALLKEQQALQTVCLK 68

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ð g Kastrup JS;

Tang YT,

Cao Y,

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The inventorial tenance to the uesayu of Linguistic putypeptides tructural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural comprise at least one tetranectin trimerising structural construct comprise at least one tetranectin trimerising structural comprise. The trimerist construct comprise at least one tetranectin trimerising structural comprises with the proviso that the heterologous molety is different from any of the fusion proteins CIIHEYNNI23, HERYNNI23, HERYNNI24, HERYNNIA4, HERYNNIAA, HERYNN
                                                                                                                                                                                                     New monomer polypeptide constructs for diagnosis and therapy - comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
                                                                                                                                                                                                                                                                                                                                                                   The invention relates to the design of trimeric polypeptides using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasminogen activation; clot lysis; fibrinolysis; tissue growth; tissue repair; haemostasis; neoplasia therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.2%; Score 79; DB 20; Length 228; 57.1%; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of chain of Tetranectin protein.
                                                                                            Holtet TL,
                                                                                                                     Thogersen HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 DLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key Location/Qualifiers Disulfide-bond 50..60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP60098 standard; protein; 182 AA.
                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 6; 110pp; English.
                                                                                            Graversen NJH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
  GRAVERSEN N J H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                             Nielsen BB,
                     HOLTET T L.
KASTRUP J S.
                                                                                                                                                            WPI; 1999-080897/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                  Etzerodt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUN-1991
                                                                                                                  Larsen IK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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GRAV/)
                                       (KAST/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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Matches
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qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, plg, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess blodiversity and for nutritional purposes. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; CIIH6FXTN123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                 R, Asundi V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.2%; Score 79; DB 22; Length 202; llarity 57.1%; Pred. No. 0.016; Conservative 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                               Chen
                                                                                                                                                                                                                                                                                                                                                               Qian XB, Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                  Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 1069; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIIH6FXTN123 fusion protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW94261 standard; protein; 228
                                                                                                                                          25-JAN-2001; 2001WO-US02687.
                                                                                                                                                                                         25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
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                                                                                                                                                                                                                                                                                                                                                            Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                             Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                                                                         2001-476164/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 16; Conserv
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                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 AA;
                                                                                                                                                                                                                                                                                                                                                          Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAH98693
                                                   WO200154477-A2.
         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-APR-1999
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                                                                                                 02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUN-1998;
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Sequence

Query Match

Matches

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AAW94261;

AAW9426

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Gaps

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5; Indels

us-09-445-576a-38.rag

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52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-APR-1999
                    Larsen IK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW94270;
                                                                                  activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW94270
   qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin.
                                                                                                                                                                                                                                     formula shown in AAP60098. Tetranectin stimulates and controls the plasminogen activation resulting in a higher rate of clot lysis or fibrinolysis, esp. in the presence of blood platelets and in the presence of a complex fibrin clot from blood. It stimulates and controls the plasminogen activation in the absence of fibrin but in the presence of a cofactor such as polylysine.
                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                              Tetranectin is comprised of four polypeptide chains having the
                                                                                                                                                                         New Tetranectin protein - purified from human blood plasma by e.g. affinity chromatography on a column with coupled kringle of plasminogen
                                                                                                                                                                                                                                                                                                                       40.4%; Score 74; DB 7; Length 182; 53.6%; Pred. No. 0.065;
                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tetranectin polypeptide fragment (residues 1-52).
                                                                                                                                                                                                                                                                                                                                         7; Mismatches
                                                                                                                                                                                                                                                                                                                                                           9 DLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                      :||::::| :| ||| ||||||||:
25 ELKSRLDTLAQEXALLKEQQALQTVCLK 52
                                                                                                                                                                                                              Claim 9; Page la; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        AAW94254 standard; Protein; 52
                                                                                                                                      Duhl Clemmensen I, Kluft C;
                           /label= M,V
                                                                                86EP-0201005
                                                                                                  85NL-0001682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97DK-0000685
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                    (NEDE ) NEDERLAND ORG TNO.
77..176
152..168
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GRAV/) GRAVERSEN N J H. (HOLT/) HOLTET T L. (KAST/) KASTRUP J S.
                                                                                                                                                        WPI; 1986-340760/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETZERODT M.
                                                                                                                                                                                                                                                                                                                                Local Similarity
tes 15; Conserv
                                                                                                                                                                                                                                                                                                      182 AA;
                  Misc-difference
Disulfide-bond
Disulfide-bond
                                                                               10-JUN-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                 11-JUN-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09856906-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUN-1997;
                                                              30-DEC-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1998
                                            EP206400-A.
                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW94254;
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETZE/)
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                AAW94254
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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural element (TSE) which is covalently linked to at least one heterologous moiety, the TTSE being capable of forming a stable complex with 2 other TTSEs, with the proviso that the heterologous moiety is different from any of the fusion proteins CIMERTWAL23, HERYANL2, HERYANL3 (AAM94261 to AAM94264). The TTSE can be used for the construction of conjugates with heterologous moieties such as a ligand binding structure, a toxin, a detectable label, an in situ activatable substance, an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer, conjugates with heterologous moiety, a cytokine, a non-proteinaceous polymer, a photo cross-linking agent, or a group facilitating conjugation of the monomer polypeptide construct to a target. They can be used as vehicles for assembling antibody fragments into oligomeric or multivalent constructs can be used for targeted gene therapy involving selective constructs can be used for targeted gene therapy involving selective constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific conjugated at the ordinanosis. The TTSE provides a stable structure which can act as a vehicle for a wide variety of conjugates. The present sequence can also be used for delivering a substance to call sequence was amplified by PCR from the plasmid clone p7746FXTN123.

This is used in the construction of E. coli expression vectors for the construction of trimerised chimneric fusion proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                  New monomer polypeptide constructs for diagnosis and therapy comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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                                                Kastrup JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 9
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Pred. No. 0.071;
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                                            Holtet TL,
Graversen NJH, HOLLL
Thogersen HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :||:::: | :|| ||| ||||| ||:
25 ELKSRLDTLAQEVALLKEQQALQTVSLK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 DLKTQVEKLWREVNALKEMQALQTVCLR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 59; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H6FXtripa fusion protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.78;
53.68;
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                                                                                        Nielsen BB,
                                                                                                                                                                       WPI; 1999-080897/07
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Best Local Similarity
Matches 15; Conserv
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us-09-445-576a-38.rag

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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein construct comprise at least one tetranectin trimerisal proteins construct comprise at least one tetranectin trimerisal ostructural construct comprise at least one tetranectin trimerisal ostructural construct comprise at least one tetranectin trimerisal structural construct comprise at least one tetranectin trimerisal ostructural constructural constructural constructural constructural constructural constructural construction of the fusion proteins CIHEFKTN123, HEFKTN123, Conjugates with heterologous moieties such as a ligand binding conjugates with heterologous moieties such as a ligand binding conjugation to a constructure, a coxin, a detectable label, an in situ activatable substance, a newsyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer. Confugation antibody fragments into oligomeric or multivalent monomer polypeptide construct to a group facilitating conjugation of the constructs can be used for targeted gene therapy involving selective constructs can be used for trargeted gene therapy involving selective constructs can be used for trargeted gene therapy involving selective contribudy to a tumour. They can also be used for prevention or treating a citized contrology to a tumour. They can also be used for prevention a substance to contrology to a tumour. They can also be used for prevention a cutoacting a cat as a vehicle for a wide variety of conjugates. The present sequence represents a HEFKTLIPA fusion protein sequence encoded by the plasmid
                                                                                                                                                                                                                                                                                                                                                             New monomer polypeptide constructs for diagnosis and therapy comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
                                                                                                                                                                                                                                                               Kastrup JS;
                                                                                                                                                                                                                                                 Etzerodt M, Graversen NJH, Holtet TL,
Larsen IK, Nielsen BB, Thogersen HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 4; 110pp; English.
                                                  98WO-DK00245.
                                                                                             97DK-0000685
                                                                                                                                   (ETZE/) ETZERODT M.
(GRAV/) GRAVERSEN N J H.
(HOLT/) HOLTET T L.
                                                                                                                                                                                                        KAST/) KASTRUP J S.
                                                                                                                                                                                                                                                                                                                  WPI; 1999-080897/07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 AA;
                                               11-JUN-1998;
                                                                                             11-JUN-1997;
  17-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                  activity
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Gaps .; 0 37.7%; Score 69; DB 20; Length 73; 53.6%; Pred. No. 0.1; vative 7; Mismatches 6; Indels Local Similarity 53.6 les 15; Conservative Query Match Best Loca Matches

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9 DLKTQVEKLWREVNALKEMQALQTVCLR 36 a

à

Search completed: April 15, 2003, 11:47:59 Job time : 29.75 secs drosophila homo sapien caenorhabdi

drosophila

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O99322 Cicer ariet
092rq4 rhizobium m
096433 glycine max
08w2e1 glycine max
08w2e1 glycine max
08w2e1 glycine max
08w2e1 glycine max
09k9r4 bacillus ha
022909 arabidopsis
09c7b9 arabidopsis
09ngx2 entamoeba h
09lhl9 arabidopsis
                                             Q9grc3 caenorhabdi
017887 caenorhabdi
015154 homo sapien
045614 caenorhabdi
Q9tzr4 caenorhabdi
Q26152 plasmodium
Q8uyv9 strawberry
08zvh4 pyrobaculum
Q9u147 homo sapien
                                                                                                                                                          0929f2 listeria in
09sirl arabidopsis
095949 homo sapien
                                                                                                                                                                                                                                                                                                                                      Ogngx1 entamoeba h
O97230 plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.1-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Tetranectin.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "tetranectin in chicken.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ271116; CAC20217.1; -.
HSSP, P05452; ITN3
InterPro; PR051304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS050015; C_TYPE_LECTIN_1; 1.
PROSITE; PS050015; C_TYPE_LECTIN_2; 1.
SEQUENCE 201 AA; 22172 MW; 7C7F235D24426AE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 13;
1.8e-07;
ches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 VSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.3%; Score 122; DB
74.3%; Pred. No. 1.8e
Live 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 VSLKMIEDLKAMIDNISQEVALLKEKQALQTVCLK
          Q9NK92
Q20060
Q26RC3
Q17887
O15154
Q45614
Q9TZR4
Q26152
Q8UYV9
Q8UYV9
                                                                                                                                                            0929F2
0951R1
09549
09M3Z2
092R04
096433
08M2E2
08W2E2
09K9R4
09K9R4
09C7B9
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                                                                                                                                                                                                                                                                                                                                       Q9NGX1
Q97230
                                                                                                                                                             16
                                                                                                                                                                                                Local Similarity 74.3
nes 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
SEQUENCE FROM N.A.
Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wewer U.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9DDD4;
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09DDD4
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Q43529 lycopersico
Q9c0b2 homo sapien
Q91m53 arabidopsis
O69287 campylobact
Q9p102 campylobact
Q9ma6 arabidopsis
Q9vm67 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9epw4 mus musculu Q28008 bos taircus Q9xz29 drosophila Q84930 trichodesmi Q8Re6 thermoanaer Q8tt21 methanosarc Q9a0u7 streptococc
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                                                                                                (without alignments)
329.675 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                April 15, 2003, 11:44:50; Search time 22.5 Seconds
                                                                                                                                                                                                                                                 671580
          GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                            36
                                                                                                                                US-09-445-576A-37
171
1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK
                                                                                                                                                                                                                                              lotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                       671580 seqs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                                          protein search, using sw model
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084930
Q8R8C6
Q8TT21
Q9A0U7
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09P102
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
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sp_phage:*
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Gaps ö us-09-445-576a-37.rspt

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Science 287:2185-2195(2000).
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                                                      Q9X229
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                                                                                                                                                          Neame P.J., Grimm D.R.;

"Mouse homolog of human CLECSF1, a cartilage derived C-type lectin.";

"Mouse homolog of human CLECSF1, a cartilage derived C-type lectin.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

HSSP; P05452; 1HTN.

InterPro: IRF001304; Lectin.C.

Pfam: PF00059; lectin.c; 1.

SMART; SM00034; CLECT; 1.

PROSITE; PS00615; C_TYPE_LECTIN.1; 1.

PROSITE; PS50041; C_TYPE_LECTIN.2; 1.
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-type lectin homolog precursor.
Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neame P.J., Boynton R.E.;
"C-type lectin homolog from bovine cartilage.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; U22298; AAC18614.1;
HSSP; P05452; ITN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                           196 AA; 22191 MW; 9AE4C809D119E852 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 · 197 C-TYPE LECTIN HOMOLOG.
197 AA; 22215 MW; AAAC4280F41AC0F4 CRC64;
O9EPW4;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
C-type lectin superfamily 1.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              028008 PRELIMINARY, PRT, 197 AA.
028008, 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 76; DB 6;
Pred. No. 0.086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
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Matches 16; Conservative
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Bovidae; Bovinae; Bos.
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es 16; Conserv
                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                          NCB1_TaxID-10090;
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                                                                                                                                                  STRAIN-ES129/SV;
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SEQUENCE
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RESULT 3 Q28008

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RC STRAIN-BERKELEN,

RA Addans N.D., Cellinker S.E., Li P.W., Foars C.A., Gocayne J.D.,

RA Addans N.D. Cellinker S.E., Li P.W., Hoskins R.A., Calle R.F.,

Addans N.D., Cellinker S.E., Li P.W., Hoskins R.A., Calle R.F.,

RA Gorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,

RA Barila J.F., Agbayani A., An H.-J., Andrews-Frankoof C.R., Baldwin D.,

RA Ballew R.W., Basu A., Baxendale J., Baytraktarolu L., Beaaley E.M.,

RA Beson K.Y., Botchan M.R., Bouck J., Brytraktarolu L., Beaaley E.M.,

RA Berkova D., Botchan M.R., Bouck J., Brytraktarolu L., Beaaley E.M.,

RA Burtis K.C., Busam D.A., Buller H., Caddeu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Denng S., Mays A.D., Dow I.D., Dlatez S.M.

RA Dockoon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Dockoon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Dockoon K., Cabrielista C.C., Ferraz C., Ferriard S., Platzis M.,

RA Gosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Dockoon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Dockoon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Bostin D., Houston K.A., Mewland T.J., Well M.-H., Ibeeywan C.,

Andria M. Kalush F., Karpen G.H., Ke Z., Kenip D., Laiz Z.,

RA Basko P., Leel Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntor R.D., Wolarry C., Morris J., Moshreii A.,

RA Brazolo M. Pittana G.S., Pan S., Pollard J., Puri V., Rese M.G.,

RA Brisson D.R., Nelson K.A., Mixon K., Wusskern D.R., Pacaleh J.M.,

RA Brazolo M., Pittana G.S., Pan B.C., Steneler F., Shen H.,

RA Wang Z.-Y., Wassarman D.A., Weinstock M., Weissenbach J.,

RA Wang Z.-Y., Wassarman D.A., Weinstock M., Weissenbach J.,

RA Wang S.-Y., Wassarman D.A., Weiner B., Wencer B., Wang S., Yao O., Zhon C., Throper M., Banney S., Whoodage T., Worle W. Don, Shila M., Shong S., Shong S., Shong S., Shong S. KLP3A protein.

KLP3A OR BCDNA:LD21B15 OR EG:BACR25B3.9 OR CG8590.

Bursophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryotoa; Neoptera; Endopterygota: Diptera; Brachycera; Muscomorpha;

Bphydroidaa; Drosophilidae; Drosophila. Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C., Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E., Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M., Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefl M., Pacleb J.M., Murphy L., Harris D., Barrell B.; "Sequencing the distal X chromosome of Drosophila melanogaster."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) PRT; 1212 AA.

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SEQUENCE
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             RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dominic B., Zehr J.P.; "Cloning sequencing and transcriptional analysis of contiguous nifHDK "Cloning, sequencing and transcriptional analysis of contiguous nifHDK operon reveals unexpected nifD, nifDK and nifK transcripts in Trichodesmium sp. IMS101."; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
Dominio B., Zani S., Chen Y.-B., Mellon M.T., Zehr J.P.;
Morganization of the nif genes of the nonheterocystous cyanobacterium
Trichodesmium sp. IMS101.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF016484; AAF82639.1;
EMBL; AF0538; AAF82639.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
MOFE protein of nitrogenase beta subunit (EC 1.18.6.1) (NIFK).
                                                                                                                            SMART; SM00129; KISC; 1.
PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
ATP-binding; Coiled coil; Hypothetical protein; Microtubules;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 512;
                                                                                                                                                                                                              35.7%; Score 61; DB 5; Length 1212; 37.1%; Pred. No. 35; Live 9; Mismatches 13; Indels
                                                                                                                                                                                       1212 AA; 135811 MW; 7ADAD60A69B1CC4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AE001424; AAF45793.1; --
EMBL; AL138972; CAB72294.1; --
EMBL; AF131219; 3KAR.
HSSP; P17119; 3KAR.
FlyBases; F9gn0011606; Klp3A.
InterPro; IPR001752; Kinesin_motor.
Pfam; PF00225; Kinesin_il.
PRINTS; PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Trichodesmium sp. (strain IMS101).
Bacteria; Cyanobacteria; Oscillatoriales; Trichodesmium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512 AA; 56936 MW; 81E4D27A75ABAEDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 VSSSMTEDAAVFGGLKNMIDGLANSYALYKPKMIALCTTCM 153
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                                                                                                                                                                                                                                                                             512 AA.
                                                                                                                                                                                                                                                               2 VSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
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46.3%; Pred. No. 18;
tive 3; Mismatches
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InterPro; IPR000118; Nitrognse_compl.
InterPro; IPR000510; Oxred_nitrognsel.
Pfam; PF00148; Oxidored_nitro; 1.
IIGRFAMS; TIGR01286; nifk; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00699; NITROGENASE_1_1; 1. PROSITE; PS00090; NITROGENASE_1_2; 1.
                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                      13; Conservative
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                                                                                                                                                                            Motor protéin.
SEQUENCE 121
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Best Local (
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                                                                                                                                                            Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter. NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Galagan J.E., Nusbeau C., Engels R., Smirnov S., Atnoor D., Brown A., FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., Liu W., Liu J., Mukhopadhayy B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Metcalf W.W., Birren B.;

"The genome of Methanosarcina acetivorans reveals extensive metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21992816; PubMed=11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen Y., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:669-700(2002).
EMBL; AE013156; AAM25253.1;
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Hypothetical protein; Complete proteome.
SEQUENCE 185 AA; 21113 MW; 7EF54897A39F8266 CRC64;
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13;
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Methanosarcinaceae; Methanosarcina.
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                                            21, Created)
21, Last sequence update)
21, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 57; DB 17;
Pred. No. 60;
185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             654 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 13;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sensory transduction histidine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 21, Created) (TrEMBLrel. 21, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :||::|||| | : | : | : | : | : | 87 NSKLKQELKNNPDSIMQSIDLLLERQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C2A / ATCC 35395 / DSM 2834;
MEDLINE=21929760; PubMed=11932238;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 SSKMFEELKNRMDVLAQEVALLKEKQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and physiological diversity.";
Genome Res. 12:532-542(2002).
EMBL; AE010723; AAM04062.1; -.
                                                                                                                             Hypothetical protein TTE2080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.3%;
48.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanosarcina acetivorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 46.2
Matches 12; Conservative
                                               01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinase; Complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AX072930; AAL77202.1; - NON_TER _{\rm I}
                                    SEQUENCE
                                                                                                                                                                                          Homeobox.
                                                                                                                                               043529
                                                                                                                               RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9C0B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                        043529
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DR
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                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                       -!- PATHWAY: TRICARBOXYLIC ACID CYCLE.
-!- SIMILARITY: BELONGS TO THE PEPCASE FAMILY.
EMBL; ABO06516; AAK33584.1; -.
InterPro; IPR001449; PEPcase.
Pfam: PP00311; PEPCASE.1.
PRINTS; PR00150; PEPCARELIS.
PROSITE; PS00781; PEPCARELIS.
PROSITE; PS00781; PEPCASE.1; 1.
PROSITE; PS00393; PEPCASE.2; 1.
Carbon dioxide fixation; Lyase; Pyruvate; Tricarboxylic acid cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                    Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Streptococcaceae; Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spernatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
       ·,
                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase) (PEPC).
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                                                                                                                                                                                                                                                                                                                                                                                                       Score 57; DB 16; Length 920;
Pred. No. 84;
3; Mismatches 4; Indels
     Indels
                                                                                                                                                                                                                                                                                                                                                                                        464EA4A309A22237 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Quanhong Y., Rihe P., Aisheng X., Xian L., Huiqin F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative transcription factor (Fragment).
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و
                                                                               920 AA.
  4; Mismatches
                                                                             PRT;
                         | :| |||:| :| || ||: |
255 SLLFRELKHREEALRQETIFLKDDQ 279
                4 SKMFEELKNRMDVLAQEVALLKEKQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                    920 AA; 104751 MW;
                                                                                                                                                                                                                                                                                                                                                                                                       33.3%;
61.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      9 ELKNRMDVLAQEVALLKE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
12;
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                                                                           Q9A0U7
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Matches
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                                                         RESULT 8
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O8S9M9
                                                                  Q9A0U7
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SEQUENCE FROM N.A.
STRAIN-CV. VFN8; TISSUE-LEAF;
MEDLINE-96231454; PubMed-8653114;
Tornero P., Conejero V., Vera P.;
"Phloem-specific expression of a plant homeobox gene during secondary phases of vascular development.";
Plant J. 9:639-648(1996).
-:- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CV. VFN8; TISSUB-LEAF;
MEDLINE-96252900; PubMed-8672818;
Gadea J., Mayda E., Conejero V., Vera P.;
"Characterization of defense-related genes ectopically expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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                                                  Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 323;
                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART: SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
DNA-binding; Homeobox; Nuclear protein.
SEQUENCE 323 AA; 36648 MW; 0F97443219DF6CCB CRC64;
  5514013FD57EC3C3 CRC64;
                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                             DB 10;
                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Plant Microbe Interact. 9:409-415(1996).
                                                                                                                                                                                                                                                                       323 AA.
                                             Score 56.5; D
Pred. No. 9.5;
                                                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           710 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.0%; Score 56.5; F
48.3%; Pred. No. 35;
tive 5; Mismatches
                                                                                                                   7 FEELKNRMDVLAQEVALLKEK-QALQTVC 34
                                                                                                                                           32
                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X94947; CAA64417.1; -
TRANSFAC; T04093; -
InterPro; IPR001356; Homeobox
InterPro; IPR00047; HTH repressr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 KMFEELKNRMDVLAQEV-ALLKEKQALQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            virold-infected tomato plants.
83 AA; 9861 MW;
                                         33.0%;
48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00031; HTHREPRESSR.
ProDom; PD000010; Homeobox; 1.
                              Ouery Match
Best Local Similarity 48.39
Matches 14; Conservative
                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0uery Match 33.09
Best Local Similarity 48.39
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00046; homeobox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
NCBI_TaxID=197;
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Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=NCTC 11168;
BEDLINE-20150913. PubMed-10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
                           Length 1970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99214069; PubMed-10196475;
Thies F.L., Karch H., Hartung H.P., Giegerich G.;
Thies F.L., Karch H., Hartung H.P., Giegerich G.;
Characterization of the encoding gene and antigenicity of the recombinant protein.";
Free 230:61-67(1999).

BMBL; V13333; CAA73776.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.2%; Score 55; DB 2; Length 857
53.8%; Pred. No. 1.4e+02;
Live 5; Mismatches 5; Indels
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             857 AA; 95442 MW; 253A7EFCE3D76487 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ATP-dependent CLP protease ATP-binding subunit.
                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                           Score 55.5; DB 10;
Pred. No. 2.7e+02;
                                                                                                                                                     776 LSTEAKEILKQRLDITLDEVCSLKEE---KTTCI 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               857 AA.
                                                                          8; Mismatches
                                                                                                                         2 VSSKMFEELKNRMDVLAQEVALLKEKQALQTVCL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003593; AAA_ATPAse.
InterPro; IPR003959; AAA_ATPAse_centr.
InterPro; IPR001270; Chaprnin_clpA/B.
InterPro; IPR004176; Clp_N.
                                                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TrEMBLrel. 07, Created)
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Pfam; PF02861; Clp_N; 2.
PRINTS; PR00300; CLPPROTEASEA.
SMART; SM00382; AAA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00870; CLPAB_1; 1. PROSITE; PS00871; CLPAB_2; 1.
                             32.5%;
38.2%;
                                                                                                                                                                                                                                                                                                                                                                                       21,
                                                                                                                                                                                                                                                                                                                                                                   07,
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002 (TrEMBLrel.
Heat shock protein.
                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Campylobacter jejuni.
                                               Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Simi
Matches 14;
                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding
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                                Query Match
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                                                                                                                                                                                                                                                                                           069287
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                                                                                                                                                                                                                                            RESULT 13
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EMBL: AC069252; AAF8655611; -. SEQUENCE 1970 AA; 225572 MW; 26896231EAAA4E97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Conway A., Gonzales A., Hansen N., Howing B., Con L., Lenz C., Li J., Liu A., Liu K., Liu S., Wahrsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Torlumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-21082932; PubMed-11214970;

MEDLINE-21082932; PubMed-11214970;

Megase T., Kituno R., Hattori A., Kondo Y., Okumura K., Ohara O.;

Prediction of the coding sequences of unidentified human genes. XIX.

The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

For large proteins in vitro.";

DNA Res. 7:347-355(2000).

EMBL: AB051538; BAB21842.1; -.

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SEQUENCE 710 AA; 81159 MW; A3EEDC21E05A6F6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brasslcales; Brassicaceae; Arabidopsis.
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                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                           KIAA1751 protein (Fragment).
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Best Local Similarity 40.79
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A Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
A Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
An Whitehead S., Barrell B.G.;
The genome sequence of the food-borne pathogen Campylobacter jejuni
Treveals hypervariable sequences.";
The genome sequence of the food-borne pathogen Campylobacter jejuni
T. Wature 403:665-668(2000).
R. Mature 403:665-668(2000).
R. BMBL; AL139075; CAB75146.1; ...
R. InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003593; AAA_ATPase.
R. InterPro; IPR004176; Clp_N.
PR Ffam; PF002661; Clp_N.
PR PRINTS; PR003601; Clp_N.
R. PRINTS; PR003601; Clp_N.
R. PRINTS; PR003601; CLPAB_1; 1.
RRSITE; PS00870; CLPAB_1; 1.
RRSITE; PS00870; CLPAB_2; 1.
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01-0CT'2000 (TrEMBLrel. 15, Last sequence update)
01-0CT'2001 (TrEMBLrel. 19, Last annotation update)
T12H1.9
T12H1.9
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; NCBL_TaxID=3702;
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SEQUENCE 857 AA; 95543 MW;
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us-09-445-576a-37.rsp

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 15, 2003, 11:44:09 ; Search time 6.5 Seconds (without alignments) 229.715 Million cell updates/sec Run on:

US-09-445-576A-37 171 1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		, Description	P43025 mus musculu	P05452 homo sapien	_	075596 homo sapien			Q9pk85 chlamydia m		Q10411 schizosacch	-		Q9kgn4 bacillus ha	Q9x1x1 thermotoga				084310	P06687 rattus norv			_	Q9hb97 rattus norv	O07643 cyanothece		P96769 actinobacil	Q9r9s0 aeromonas p	P31230 mus musculu	m	Q9m7j4 nicotiana t	. P07390 saccharomyc	P15052 thiobacillu	· P34237 saccharomyc	Q9ulv0 homo sapien
SUMMARIES		D	TETN_MOUSE	TETN_HUMAN	TETN_CARSP	CLF1_HUMAN	YJD7_YEAST	YE33_SYNY3	VATA_CHLMU	POLG_HRV14	YD86_SCHPO	ELAD_ECOLI	NIFK_RHISN	SYS_BACHD	RA50_THEMA	A1A3_CHICK	MCA1_CRIGR	NIFK_BRASP	VATA_CHLTR	A1A3_RAT	NIFK_HERSE	PARA_HUMAN	PARA_MOUSE	PARA_RAT	NIFK_CYAA5	DYHC_NEUCR	YHBJ_ACTAC	YADS_AERPU	MCA1_MOUSE	DNAK_PORPU	MFP1_TOBAC	PT94_YEAST	NIFK_THIFE	YKR9_YEAST	MY5B_HUMAN
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R132_BRANA	ISPG_BACSU	NFL_XENLA	Y419_HUMAN	A1A3_OREMO	YP73_CAEEL	PFD4_YEAST	YA80_HAEIN	Y816_METJA	YO4P_BPT4	ATF4_HUMAN	SYS_BACSU
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206	377	544	991	1010	4385	129	257	297	333	351	425
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49	4					4	7				

ALIGNMENTS

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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-88107595; PubMed-3427041; Fuhlendorff J., Clemmensen I., Magnusson S.; Fuhlendorff J., Clemmensen I., Magnusson S.; Fuhlany structure of tetranectin, a plasminogen kringle 4 binding plasma protein: homology with asialoglycoprotein receptors and cartillage proteoglycan core protein."; Biochemistry 26:6757-6764(1987).
                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (Rel. 09, Created)
1-NOV-1993 (Rel. 25, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Tetranectin precursor (TN) (Plasminogen-Kringle 4 binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wewer U.M., Albrechtsen R.; "Tetranectin, a plasminogen kringle 4-binding protein. Cloning and gene expression pattern in human colon cancer."; tab. Invest. 67:253-262(1992).
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                  BY SIMILARITY.

TETRANECTIN.

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BY SIMILARITY.

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LT -> VI (IN REF. 2).

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A -> R (IN REF. 2).

W, 639E7334D59EB04E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sorensen C.B., Berglund L., Petersen T.E.; "Cloning and mapping of the murine tetranectin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 22-202, AND VARIANTS SER-55 AND MET-58.
                                                                                                                                                                                             Query Match 100.0%; Score 171; DB 1; Best Local Similarity 100.0%; Pred. No. 3.1e-14; Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                     1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
                                                                                                                                                                                                                                                38 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 73
                                                                                                                                                                                                                                                                                                          202 AA
                                                                                                                                                                                            100.0%; Score 171;
     InterPro; IPR001304; Lectin_C.
Pfam, PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Plasma; Signal.
SIGNAL.
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SEQUENCE FROM N.A.
MEDLINE-92380263; PubMed=1511740;
Berglund L., Petersen T.E.;
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MEDLINE-92365345; PubMed-1354271;
                                                                                                                                                                        22257 MW;
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 MGD; MGI:104540; Tna.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE=973893836). PubMed=9256258.
Nielsen B.B., Kastrup J.S., Rasmussen H., Holtet T.L., Graversen J.H., Etzerodt M., Thoegersen H.C., Larsen I.K.;
Etzerodt M., Thoegersen H.C., Larsen I.K.;
Etzerodt M., Thoegersen H.C., Larsen I.K.;
Fystal structure of tetranectin, a trimeric plasminogen-binding protein with an alpha-helical coiled coil.";
FBSS Lett. 412:388-396(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 66-202.
MEDLINE-98437604; PubMed-9757090;
Kastrup J.S., Wielsen B.B., Rasmussen H., Holtet T.L., Graversen J.H.,
Etzerodt M., Thoegersen H.C., Larsen I.K.;
"Structure of the C-type lectin carbohydrate recognition domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human terranectin.";
Acta Crystallogr. D 54:757-766(1998).
-!- FUNCTION: Tetranectin binds to plasminogen and to isolated kringle
4. May be involved in the packaging of molecules destined for
                                                                                                                                 Jaquinod M., Holtet T.L., Etzerodt M., Clemmensen I., Thoegersen H.C., Roepstorff P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: Homotrimer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: MW-20535.8; MW_ERR-2.4; METHOD-Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM0034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
Lectin; Plasma; Signal; Polymorphism; Glycoprotein; 3D-structure.
                                                                                                                                                                                                                                                  "Mass spectrometric characterisation of post-translational modification and genetic variation in human tetranectin."; Biol. Chem. 380:1307-1314(1999).
PARTIAL SEQUENCE, MASS SPECTROMETRY, AND VARIANT GLY-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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V -> M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TETRANECTIN.
C-TYPE LECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X70911; CAA50265.1; JOINED. EMBL; X70912; CAA50265.1; JOINED. EMBL; X40912; CAA50265.1; JOINED. EMBL; X64559; CAA45860.1; -... EMBL; X98121; CAA66803.1; -... EMBL; X98121; CAA66803.1; -... PIR; A29747; R29747. PIR; S19865; S19865. PIR; S19865; S
                                                                                                      MEDLINE-20080486; PubMed-10614823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X70910; CAA50265.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202
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                                                TISSUE-Plasma;
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SIGNAL
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-type lectin superfamily member 1 precursor (Cartilage-derived C-type lectin).
CLECSF1.
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Blasmobranchii; Galeomorphii; Galeoidea; Carcharhinidae; Carcharhinus.
Carcharhinidae; Carcharhinus.
                                                                                                                                                                                                                                                          to the mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 166;
                                                                                                                                                                                                                        Score 89; DB 1; Length 166
Pred. No. 0.00032;
5; Mismatches 9; Indels
                                               Indels
      /FTId=vAR_012318.
2B0DCB5DF22E1AB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      18432 MW; 53EF812DEA5C6119 CRC64;
                                      Pred. No. 3.7e-11;
6; Mismatches 1;
                               Score 146; DB 1;
                                                                                                                                  01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-LUN-2002 (Rel. 41, Last annotation update)
Tetranectin-like protein.
                                                                       38 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 73
                                                             1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
                                                                                                                     166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 AA
                                                                                                                                                                                                                                                                                                                                                        C-TYPE LECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 SGKGKDDLRNEIDKLWREVNSLKEMOALOTVCLK 39
                                                                                                                                                                                                                                                                                                                              PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                   Carcharhinus springeri (Reef shark).
S -> G.
                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                        InterPro; IPR001304; Lectin_C.
               22567 MW;
                               85.4%;
                                                                                                                                                                                                                                                                                                                                                                                                     52.0%;
58.8%;
                                                                                                                                                                                                                                                                                                              Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                     64 1
136 1
166 AA;
                                     Best Local Similarity
Matches 29; Conserve
               202 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                               Lectin; Cartilage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                   TETN_CARSP
P26258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLF1_HUMAN
075596;
                                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
SEQUENCE
               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              DISULFID
                               Query Match
                                                                                                                                                                                                                   SEQUENCE
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VARIANT
                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                            TETN_CARSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLF1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                 Neame P.J., Tapp H., Grimm D.R.;
"The cartilage-derived, C-type lectin (CLECSFI): structure of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-TYPE LECTIN SUPERFAMILY MEMBER 1. C-TYPE LECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pohl T.M., Aljinovic G.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUIAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: STRONG, TO YEAST YJL038W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 33, Last sequence update)
(Rel. 40, Last annotation update)
24.8 kDa protein in NSP1-TAD2 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                               and chromosomal location.";
Blochim. Blophys. Acta 1446:193-202(1999).
-! TISSUE SPECIFICITY: Restricted to cartilage.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB924DBDDB7729A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 72; DB 1;
Pred. No. 0.047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00615; C_TYPE_LECTIN_1; 1. PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 ELKNRMDVLAQEVALLKEKQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF077345; AAD12542.1; -. EMBL; AF077344; AAD12542.1; JOINED.
TISSUE=Cartilage;
MEDLINE=99453719; Pubmed=10524194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P05452; 1HTN.
Genew: HGNN:2052; CLECSF1.
InterPror; PF0001304; Lectin_C.
Ffam: PF00059; lectin_C; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequal 16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22232 MW;
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57.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
197
192
78
191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XJL037W OR J1234.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lectin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical
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P47056;
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DISULFID
DISULFID
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591 AA.

PRT;

STANDARD;

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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
V-type ATP synthase alpha chain (EC 3.6.3.14) (V-type ATPase subunit
                                                                                                                        Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
                                                                                                            ATPA OR TC0582.
                                                                                                                                                                                      STRAIN-MoPn
                     VATA_CHLMU
Q9PK85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97061201; PubMed-8905231; Ranaka A., Asamizu E., Nakamura Y., Ranako T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Vokumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Tabata S.; "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; I. SIMILARITY: BELONGS TO THE UPF0031 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                32.2%; Score 55; DB 1; Length 224; 44.4%; Pred. No. 6.7; tive 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: D90913; BAA18311.1; -.

InterPro; IPR000631; UPF0031.

InterPro; IPR004443; YjeF_Nterm.

Pfam: PF01256; UPF0031; 1.

TIGRFAMS; TIGR00196; YjeF_cterm; 1.

R TIGRFAMS; TIGR00197; YjeF_nterm; 1.

R PROSITE; PS01049; UPF0031.1; 1.

R PROSITE; PS01049; UPF0031.2; 1.

W Hypothetical protein; Complete proteome.

SEQUENCE 524 AA; 55225 MW; 7E1527990b4133D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 55; DB 1; Length 524;
Pred. No. 16;
                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                            POTENTIAL.
6C17841176EADC1F CRC64;
                                                                                                                                                                                                                                                                                                                                              Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein sll1433.
                                                                                                                                                                                                                                                            524 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQT 32
                                                    POTENTIAL. POTENTIAL.
                                                                                                                                                                              Transmembrane.
                                                                                                                                                                2 VSSKMFEELKNRMDVLAQEVALLKEKQ 28
                                                            175 195 P
200 220 P
224 AA; 24746 MW;
            EMBL; Z49312; CAA89328.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.28;
                                                                                                                          Local Similarity 44.4 nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Conservative
                                                                                                                                                                                                                                                          STANDARD;
                                                  29
195
220
                         S0003574; YJL037W
                                    Hypothetical protein;
TRANSMEM 9 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1148;
                                                                                                                                                                                                                                                        YE33_SYNY3
P74217;
                                                            TRANSMEM
TRANSMEM
SEQUENCE
                                                                                                                  Query Match
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                                 STRAIN-MOPn / Nigg;
MeDLINB-20150525; PubMed-10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLG_HRV14 STANDARD; PRT; 2179 AA.
POLG_HRV14 STANDARD; Q84735; Q84739; Q84740;
PO3303; Q82041; Q89763; Q89883; Q84774; Q84775; Q84776; Q84777;
Q89649; Q84778; Q84779;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 11, Last annotation update)
Genome polyprotein [Contains: Coat proteins VPI TO VP4; Core proteins P2A TO P2C, P3A; Genome-linked protein VPG; Picornain 3C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 28:1397-1406(2000).

-!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE V-TYPE ALPHA CHAIN IS A CATALYTIC SUBUNIT.

-!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00006; ATP-synt_ab. 1.
Pfam; PF000306; ATP-synt_ab.; 1.
Pfam; PF02874; ATP-synt_ab_N; 1.
PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
Hydrolase; ATP synthesis; Hydrogen ion transport; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                   "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 32.2%; Score 55; DB 1; Length 591; Best Local Similarity 34.5%; Pred. No. 18; Matches 10; Conservative 8; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (POTENTIAL).; 7F8432BAB0741B14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000793; ATPase_a/bC.
InterPro; IPR004100; ATPase_a/bN.
InterPro; IPR00194; ATPase_a/bcentre.
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92 IFDGLQNRLEVLADTSLFLKRGEYVNAIC 120
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65301 MW;
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SEQUENCE FROM N.A.
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NP_BIND 242
SEQUENCE 591 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         þe
                                                         Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-85140171; PubMed-2983312;
Callahan P.L., Mizutani S., Colonno R.J.;
Molecular cloning and complete sequence determination of RNA genome of human rhinovitus type 14.";
Proc. Natl. Acad. Sci. U.S.A. 82:732-736(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNITS, EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VP1, VP2, VP3, AND VP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
MEDLINE-85296372; PubWed=2993920;
Rossman M.G., Arnold E., Erickson J.W., Frankenberger E.A.,
Griffith J.P., Hecht H.-J., Johnson J.E., Kamer G., Luo M.,
Mosser A.G., Rueckert R.R., Sherry B., Vriend G.;
"Structure of a human common cold virus and functional relationship
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEKSE.
--- CATALYTIC ACTIVITY: Selective cleavage of Gln-|-dly bond in the pollovirus polyprotein. In other picornavirus reactions Glu may substituted for Gln, and Ser or Thr for Gly.
--- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS. SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3. CAUTION: THE PBB DATA BANK COWTAINS THE 3D-STRUCTURE COORDINATE OF PROTEINS VPI, VP2, VP3, AND VP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Analysis of the structure of a common cold virus, human rhinovirus 14, refined at a resolution of 3.0 A."; J. Mol. Biol. 211:763-801(1990).
-i- FUNCTION: P3C POLYBEPTIDE IS A PROTEASE THAT CLEAVES AT CERTAIN
(EC 3.4.22.28) (Protease 3C) (P3C); RNA-directed RNA polymerase P3D
(EC 2.7.7.48)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arnold E., Rossman M.G., "The use of molecular-replacement phases for the refinement of the
                                                                                                                                                           MEDLINE-85037949; PubMed-6093056; Stanway G., Hughes P.J., Mountford R.C., Minor P.D., Almond J.W. "The complete nucleotide sequence of a common cold virus: human
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=91188162; PubMed=8383233;
Lee W.M., Monroe S., Rueckert R.R.;
"Role of maturation cleavage in infectivity of picornaviruses: activation of an infectosome.";
"Virol. 67:2110-2122(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
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MEDLINE=90189144; PubMed=2156077;
                                                                                                                                                                                                                                            Wucleic Acids Res. 12:7859-7875(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human rhinovirus 14 structure.";
Acta Crystallogr. A 44:270-282(1988);
                                    Human rhinovirus 14 (HRV-14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; K02121; AAA45756.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to other picornaviruses.";
Nature 317:145-153(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arnold E., Rossman M.G.;
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                               NCBI_TaxID=12131;
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                                                                                                                                                                                                                           chinovirus 14
                                                                                Rhinovirus
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Pfam; PF01552; Pico_P2B; 1.
Pram; PF0226; Pico_P1A; 1.
Probom; P0001125; Cys_Protease-3C; 1.
Probom; P0001125; Cys_Protease-3C; 1.
Probom; P0001306; Pico_P2B; 1.
Probom; P0001306; Pico_P2B; 1.
Polyprotein; Coat protein; Core protein; Transferase;
RNA-directed RNA polymerase; Hydrolase; Thiol protease; Myristate;
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PROTEASE (POTENTIAL).
PROTEASE (POTENTIAL).
P -> L (IN REF. 3).
P -> H (IN REF. 3).
P -> KS (IN REF. 3).
EWD -> KS (IN REF. 3).
C -> R (IN REF. 3).
NP -> KS (IN REF. 3).
NP -> KS (IN REF. 3).
NP -> KS (IN REF. 3).
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COAT PROTEIN VP2 (P1B).
COAT PROTEIN VP3 (P1C).
COAT PROTEIN VP1 (P1D).
CORE PROTEIN P2A.
CORE PROTEIN P2A.
CORE PROTEIN P2C.
CORE PROTEIN P2C.
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InterPro; IPR001138; Pico_PIA.
InterPro; IPR000081; Pico_P2A.
InterPro; IPR002527; Pico_P2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam: PF00073; rhv; 3.
Pfam: PF00548: Cys. protease-3C; 1.
Pfam: PF00560; RNA_dep_RNA_pol; 1.
Pfam: PF00910; RNA_helicase; 1.
Pfam: PF00947; Pico_P2A: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR000605; RNA_helicase.
Interpro; IPR001205; RNA_pol_P3D.
Interpro; IPR001676; Rhv
X01087; CAA25565.1;
L05355; AAA45758.1;
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1RUG; 14-NOV-95.
1RUH; 14-NOV-95.
1RUJ; 14-NOV-95.
1RUJ; 14-NOV-95.
1RVF; 25-FEB-98.
                                                  4RHV; 15-OCT-94.
1RMU; 15-OCT-94.
2RMU; 15-OCT-94.
                                                                                                                 2R05; 15-0CT-94.
2R06; 15-0CT-94.
1R08; 15-0CT-94.
1R08; 15-0CT-94.
1R09; 15-0CT-94.
2RR1; 15-0CT-94.
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14-NOV-95.
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01-NOV-94.
01-NOV-94.
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                                  A03901; GNNYH4
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MEROPS; C03.UPB;
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2RS5;
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PDB;
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                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=K1Z / MG1655,
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                 ELAD_ECOLI STANDARD; PRT; 402 AA.
047013; P76480;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-DCT-2001 (Rel. 40, Last annotation update)
16-DCT-2001 (Rel. 40, Last annotation update)
18-DCT-2001 (Rel. 40, Last annotation update)
18-DCT-101 (Rel. 40, Last annotation update)
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Pred. No. 81;
6; Mismatches 3; Indels
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1957 AA; 222785 MW; 3F480CA06171D9DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                               EMBL; 270690; CAA94624.1; -.
                                                                                                                                                                                                                                                                                                               31.6%;
50.0%;
                                                                                                                                                                                                  Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                              Query Match 31.6
Best Local Similarity 50.0
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huisman G.W.;
                                                                                                                                                                                                                                                                                       Hypothetical
SEQUENCE 19
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                                  33.
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                                  2 AND
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                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                  REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein C1F3.06c in chromosome I
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                                                                                                                                                                                                                                                                                                                                                                          Pred. No
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  NCBI_TaxID-4896
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Q10411;
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L-seryl-tRNA(Ser).
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                                                                                                                                                                                  Multigene family
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Q9KGN4;
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Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
Perret X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Badenoch-Jones J., Holton T.A., Morrison C.M., Scott K.F., Shine a "Structural and functional analysis of nitrogenase genes from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular basis of symbiosis between Rhizobium and legumes."; Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1990 (Rel. 16, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1997 (Rel. 38, Last annotation update)
Nitrogenase molybdenum-iron protein beta chain (EC 1.18.6.1)
(Nitrogenase component I) (Dinitrogenase).
(NIFKI OR YAVM) AND (NIFK2 ON X4XC).
Rhizobium sp. (Strain NGR234).
                                                                                                                                                                                                                                      31.3%; Score 53.5; DB 1; Length 402; 37.1%; Pred. No. 19;
          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                             14; Indels
                                                                                                                                                                                                      Q -> QQ (IN REF. 1).
; 6CA5C307F5DFCEE8 CRC64;
                                                                                                                                                                                                                                                                                                513 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                broad-host-range Rhizobium strain ANU240.";
Gene 77:141-153(1989).
                                                                                                                                                                                                                                                                                  1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCL 35
                                                                                                                                                                                                                                                           7; Mismatches
                                                                                                                                  EMBL; U58768; AAB02733.1; -.
EMBL; AE000316; AAC75329.1; ALT_INIT.
EcoGene; EG14261; elaD.
                                                                                                                                                                    InterPro, IPR003653; SUMO_protease.
Pfam; PF02902; Peptidase_C48; 1.
                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-ANU 240;
MEDLINE-89306671; PubMed-2744485;
                                                                                                                                                                                                              402 AA; 45947 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 132-195 FROM N.A.
                                                                                                                                                                                                                                                             13; Conservative
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid sym pNGR234a.
                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                            Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                               NIFK_RHISN
P19067;
                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                   NIFK_RHISN
                                                                                                                                                                                                                                                           Matches
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Nucleic Acids Res. 28:4317-4331(2000).
-!- CATALYTIC ACTIVITY: ATP + L-serine + tRNA(Ser) = AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNTT: Homodiner (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000510; Oxred_nitrognsel.
Pfam; PF00148; oxidored_nitro; 1.
TIGRPAMS; TIGR01286; nifk; 1.
PROSITE; PS00699; NITROGENASE_1_1; 1.
PROSITE; PS00090; NITROGENASE_1_2; 1.
Oxidoreductase; Nitrogen fixation; Molybdenum; Iron-sulfur; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Seryl-tRNA synthetase (EC 6.1.1.11) (Serine--tRNA ligase) (SerRS).
SERS OR BH0024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Masui N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., M.
Euji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                513 AA; 57302 MW; 41631040335541AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VSSKMFEE-----LKNRMDVLAQEVALLKEKQ-ALQTVCL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           425 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.3%; Score 53.5; 141.5%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002106; AAtRNA_ligaseII.
InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR002317; tRNA-synt_ser.
                                                                                                                                                                  EMBL; AE000102; AAB91901.1; -
EMBL; AE000105; AAB91925.1; -
PIR; PS0046; PS0046.
HSSP; P07329; ANIN.
InterPro; IPR000318; Nitrognse_compl.
InterPro; IPR000510; Oxred_nitrognsel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; Pubmed-11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00587; tRNA-synt_2b; 1.
Pfam; PF00403; SeryL-KRNA_N; 1.
PRINTS; PR00981; TRNASYNTHSER.
TIGRFAMS; TIGR00414; serS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AP001507; BAB03743.1; --
                                                                                                                                     EMBL; M26963; AAA26327.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 41.5
nes 17; Conservative
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A1A3_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-MSBB / DSM 3109;
MEDLINE-99287316; PubMed-10360571;
MEDLINE-99287316; PubMed-10360571;
Haft D. H., Hickey E. K. A. Gill S. R., Gwinn M. L., Dodson R. J.,
Hackey E. K. A. Garten M. C., Ketchum K. A.,
McDonald L., Utterback T. R., Malek J. A., Linher K. D., Garrett M. M.,
Stewart A. M., Cotton M. D., Fratt M. S., Phillips C. A., Richardson D.,
Heldelberg J., Sutton G. G., Fleischmann R. D., Eisen J. A., White O.,
Salzberg S. L., Smith H. O., Venter J. C., Fraser C. M.,
Genome sequence of Thermotoga maritima.";
Paridence for lateral gene transfer between Archaea and Bacteria from
Nature 399:323-339(1999).
PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mrell by unwinding and/or repositioning DNA ends into the mrell active site (By
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR03395; SMC_N.
Pfam; PF02463; SMC_N: 1.
DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.
NP BIND 37 ATP (BY SIMILARITY).
                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Forms a complex with mrell (By similarity). SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
                                                                                             Score 52; DB 1; Length 425;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                          Thermotoga maritima.
Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                      425 AA; 48541 MW; DB4F2EDA0EEDE676 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (BY SIMILARITY),
COILED COIL (POTENTIAL),
W; 31BA9F72A4EC5CD2 CRC64;
                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable DNA double-strand break repair rad50 ATPase.
RAD50 OR TM1636,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                            852 AA.
                                                                                                                                6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.
                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 SKMFEELKNRMDVLAQEVALLKEKQ 28
                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                            8 EELKNRMDVLAQEVALLKEKQ 28
                                                                                                                                                                                 |||||:|:::||||||:::
| 46 EELKSRRNQVSQEVAQLKREK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              852 AA; 100001 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001806; AAD36703.1; -.
TIGR; TM1636; -.
                                                                                           30.4%;
                                                                                                          1 Similarity 52.4%;
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40,
                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                     Complete proteome
SEQUENCE 425 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity)
                                                                                                                                                                                                                                                                                    RA50_THEMA
09X1X1;
                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                   RASO_THEMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sodium/potassium_transport; Transmembrane; Phosphorylation;
Metal-binding; ATP-binding; Multigene family.
1 74 CYTOPLASMIC (POTENTIAL).
                                                                 chain (EC 3.6.3.9)
                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
(E1-E2 ATPASES). SUBFAMILY IIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LUMENAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
LUMENAL (POTENTIAL).
                    01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last anotation update)
Sodium_potassium transporting Arpase alpha-3 che
(Sodium pump 3) (Na+/K+ Arpase 3) (Alpha(III)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LUMENAL (POTENTIAL).
  1010 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P04191; IEUL.
InterPro: IPR001757; ATPase_E1-E2.
InterPro: IPR004014; GALIOn_ATPasse.
InterPro: IPR00661; H/K.Na/K_ATPasse.
InterPro: IPR001454; H1gnase/hydrlase.
Pfam; PF00122; B1-E2_ATPasse. 1.
Pfam; PF00689; Cation_ATPasse_C: 1.
Pfam; PF00689; Cation_ATPasse_C: 1.
Pfam; PF00702; Hydrolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0119; CATATPASE.
PRINTS; PRO0121, NAKATPASE.
TIGREAMS; TIGRO1106; X K ATPASE_alp; 1.
PROSITE; PS00154; ATPASE_E1_E2; 1.
                                                                                                                                                                                    MEDLINE-91023019; PubMed-2171348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M59960; AAA48982.1; -.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95
118
139
139
275
295
307
325
779
779
779
789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; B37227; B37227.
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                 NCBI_TaxID=9031;
A1A3_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
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POTENTIAL.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quevillon S., Agou F., Robinson J.-C., Mirande M.;
Quevillon S., Agou F., Robinson J.-C., Mirande M.;
The p43 component of the mammalian multi-synthetase complex is likely
to be the precursor of the endothelial monocyte-activating polypeptide
II oytokine.,
J. Biol. Chem. 272:32573-32579(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBDNIT: COMPONENT OF THE MULTISYNTHETASE COMPLEX WHICH IS COMPRISED OF A BIFUNCTIONAL GLUTAMYL-PROLYL-TRNA SYNTHETASE, THE MONOSPECIFIC ISOLEUCYL, LEUCYL, GLUTAMINYL, METHIONYL, LYSYL, ARGINYL, AND ASPARTYL-TRNA SYNTHETASES AS WELL AS THREE AUXILIARY
                                                                                                                                PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY PKA) (BY SIMILARITY)
BINDING OF PHOSPHOINOSITIDE-3 KINASE (BY
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                         16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Multisynthetase complex auxiliary component p43 [Contains:
Endothelial-monocyte activating polypeptide II (EMAP-II) (Small inducible cytokine subfamily E member 1)].
                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                 Score 52; DB 1; Length 1010; Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.8%; Score 51; DB 1; Length 359; 61.1%; Pred. No. 34;
                                                                                                                                                                                          MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
W; 71526BC25633BFA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                   CYTOPLASMIC (POTENTIAL)
                           LUMENAL (POTENTIAL).
                                                                                        LUMENAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 359 AA
                                                                                                                                                                                                                                                                               7; Mismatches
                                                                         POTENTIAL.
                                            POTENTIAL.
                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                             11 KNRMDVLAQEVALLKEKQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98070438; PubMed=9405472;
                                                                                                                                                                                                                       111284 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEINS, P18, P48 AND P43
                                                                                                                                                                                                                                                    30.4%;
38.5%;
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                 363
930
                                                                                                                                                                                                                       1010 AA;
                                                                                                                                                                                                                                                                   Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cricetulus.
NCBI_TaxID=10029;
                                                                                                                                                                                                                                                                                                                                                                                                            MCAl_CRIGR
O54873;
                                                                                                                                                                                                                                                                               10;
 DOMAIN
TRANSMEM
                                                                                                                                                                                                                       SEQUENCE
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MOD_RES
MOD_RES
BINDING
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                                            FRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
MCA1_CRIGR
                                                                                                                                                                                             METAL
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Search completed: April 15, 2003, 11:48:32 Job time: 8.5 secs

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us-09-445-576a-37.rpr

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 15, 2003, 11:45:44; Search time 11.75 Seconds Run on:

(without alignments) 294.540 Million cell updates/sec

36 US-09-445-576A-37 171 1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

PIR_73:* Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

		æ			SUMMAKIES	
Result No.	Score	Query	Length	DB	ID	Description
-	171	100.0	202	~	JC4031	tetranectin precur
7	146	85.4	202	7	TTHUN	
m	88	52.0	166	٦	A37289	
4	56.5	33.0	323	7	T07734	0
S	52	32.2	224	7	856809	probable membrane
9	52	32.2	524	7	575852	hypothetical prote
7	52	32.2	591	~	E81687	-
80	52	ď	857	7	F81396	
6	52	ä	2179	ч	GNNYH4	qenome polyprotein
10	54	31.6	761	7	T03719	probable thyroid r
11	54	ä	1549	7	T21809	hypothetical prote
12	54	•	1893	~	T22661	
13	54		1957	~	T38077	
14	54		2823	7	T23064	hypothetical prote
15	54		2823	7	F87908	protein T22A3.8 [i
16	54		3102	7	T43291	laminin alpha chai
17	53.5		403	7	C64998	hypothetical prote
18	53.5	31.3	513	~	T10830	_
19	ë.	31.3	-	~	T30840	serine-repeat anti
20	53	31.0		~	AH1722	hypothetical prote
21	53	31.0	_	N	A84647	hypothetical prote
22	52	30.4	_	~	T08831	. disease resistance
23	52	30.4	213	7	E83972	hypothetical prote
24	52	30.4	425	~	H83652	\sim
25	52	30.4	486	7	B84914	, hypothetical prote
56	52	30.4		~	AB3288	¥
27	52	30.4	852	ď	D72230	conserved hypothet
28	2	30.4	1010	~	B37227	Na+/K+-exchanging
29	51.5	30.1	381	~	A54415	transcription fact

RESULT 2

tetranectin precursor [validated] - human
N;Alternate names: plasminogen-kringle 4 binding protein
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Species: Homo sapiens
C;Species: Homo sapiens
C;Species: Homo sapiens
C;Accession: S34126; A56835; A29747; I38359; S19865
R;Berglund, L.; Petersen, T.E.
FEBS Lett. 309, 15-19, 1992
A;Title: The gene structure of tetranectin, a plasminogen binding protein.
A;Reference number: S24126; MUID:92380263; PMID:1511740
A;Accession: S24126
A;Molecule type: DNA
A;Residues: 1-202 <BER>
A;Cross-references: EMBL:X70911
R;Wewert, U.M.; Albrechtsen, R.
Lab. Invest. 67, 253-262, 1992
A;Title: Tetranectin, a plasminogen kringle 4-binding protein. Cloning and gene expre A;Accession: A56835; MUID:92365345; PMID:1354271
A;Accession: A56835
A;Molecule type: mRNA
A;Residues: 1-202 <WEW>

probable sulfatase probable sulfatase	maltose ABC transp hypothetical prote	MADS box protein m conserved hypothet	nitrogenase (EC 1. probable ATP synth	Na+/K+-exchanging hypothetical prote	fatty-acid synthas conserved hypothet	protein kinase hom dynein heavy chain	conserved hypothet endothelial monocy
E91023 F85867	H72205 T43093	S46526 AI0458	B23874 B71531	C24639 T25808	T18200 C70438	T02456 B54802	E86899 A55053
77	00	7 7	7	0 0	7 7	77	44
407	833 69	219	513 591	1013	2342	799	90 310
30.1	30.1 29.8	29.8 29.8	29.8 29.8	29.8 29.8	29.8	29.5	29.2 29.2
51.5	51.5 51	51 51	51	51	51.5	50.5	50
30 31	32 33	34 35	36 37	38 39	40	42	44 45

ALIGNMENTS

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Chacesion: JC4011
Riscension: JC
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                                                                  C;Species: Mus musculus (house mouse)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 3.6e-14;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
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tetranectin precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38
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us-09-445-576a-37.rpr

1;

Gaps

6 DB 2;

Length 323;

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probable membrane protein YJL037w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein J1234
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 19-Apr-2002
C;Accession: S56809
R;Pohl, T.M.; Aljinovic, G
R;Pohl, T.M.; All
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
875852
System of the control of the contro
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A;Residues: 1-524 (KAN>
A;Cross-references: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN:BAA18311.1; PID:g165
A;Cross-references: EMBL:D90913; GB:AB001339; AID:g1653348; PIDN:BAA18311.1; PID:g165
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Thermotoga maritima hypothetical protein MTH1256
A; Molecule type: mRNA
A; Residues: 1-323 <TOR>
A; Residues: 1-323 <TOR>
A; Cross-references: EMBL:X94947; NID:g1161574; PIDN:CAA64417.1; PID:g1161575
A; Experimental source: cultivar VFN8; leaf
C; Genetics:
A; Gene: VAHOXI
A; Introns: 49/3; 178/3
A; Note: specifically expressed in the phloem during phases of secondary growth
C; Superfamily: unassigned homeobox, proteins; homeobox homology
C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
F; 88-144/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: S75852
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55; DB 2; Length 524;
Pred. No. 34;
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A;Reference number: S74322; MUID:97061201; PMID:8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 55; DB
Pred. No. 14;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.0%; Score 56.5; 48.3%; Pred. No. 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 KMFEELKNRMDVLAQEV-ALLKEKQALQT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VSSKMFEELKNRMDVLAQEVALLKEKQ 28
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C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.2%;
ilarity 44.4%;
Conservative
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A;Cross-references: SGD:S0003574
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Best Local Similarity
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nes 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Matches 1
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Matches
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S56809
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                          A; Experimental source: placenta
R; Fuhlendorff, J.; Clemmensen, I.; Magnusson, S.
Blochemistry 26, 6757-6764, 1987
A; Title: Primary structure of tetranectin, a plasminogen kringle 4 binding plasma protei
A; Reference number: A29747; MUID:88107595; PMID:3427041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           terrancetin homolog - reef shark
C;Species: Carcharhinus springeri (reef shark)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A37289, A37287
R;Neame, P.J.; Young, C.N.; Treep, J.T.
R;Neame, P.J.; Young, C.N.; Treep, J.T.
Protein Sci. 1, 161-168, 1992
A;Title: Primary structure of a protein isolated from reef shark Carcharhinus springeri
A;Reference number: A37289; MUID:93284081; PMID:1304877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RiTornero, P.; Conejero, V.; Vera, P. Blant J. 9, 639-648, 1996
A;Title: Phloem-specific expression of a plant homeobox gene during secondary phases of A;Reference number: 216103; MUID:96237454; PMID:8653114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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C;Species: Lycopersicon esculentum (tomato)
C;Date: 14-May_1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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        A; Cross-references: EMBL: X64559; NID: 937408; PIDN: CAA45860.1; PID: 937409
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Pred. No. 4.9e-11;
6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.0%; Score 89; DB 1; Length 166; 58.8%; Pred. No. 0.00056; Live 5; Mismatches 9; Indels
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F;37-160/Domain: C-type lectin homology <LCH>
F;37-47,64-160,136-152/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: T07734
A;Status: prellminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: tetranectin; C-type lectin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 73
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Best Local Similarity 58.8<sup>†</sup>
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 80.6 Matches 29; Conservative
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Mismatches

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Conservative

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Matches

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N;Contains: coat protein VP1; coat protein VP2; coat protein VP3; coat protein VP4; c RNA-directed RNA polymerase (EC 2.7.7.48)
C;Specias: human rhinovirus 14
C;becias: human rhinovirus 14
C;becias: bereb-1985 #sequence_revision 25-Feb-1985 #text_change 05-Jun-1998
C;Accession: A03901
                                                                                                                                                                                                                                                                                                                                  Ristanway, G.; Hughes, P.J.; Mountford, R.C.; Minor, P.D.; Almond, J.W.

Nucleic Acids Res. 12, 7859-7875, 1984

A;Title: The complete nucleotide sequence of a common cold virus: human rhinovirus 14

A;Reference number: A03901; MUID:85037949; PMID:6093056

A;Recession: A03901; MUID:85037949; PMID:6093056

A;Recession: A03901; MUID:85037949; PMID:6093056

A;Recession: A03901

A;Recession: A03901; MUID:85037949; PMID:60protein

C;Reywords: genomic RNA

A;Residues: 1-2179 <STA>

C;Superfamily: poliovirus genome polyprotein

C;Reywords: genome-linked protein; nucleotidyltransferase; phosphoprotein

C;Reywords: genome-linked protein vP2 *status predicted <vP2>

F;1-69/Product: coat protein vP3 *status predicted <vP3>

F;568-856/Product: coat protein vP1 *status predicted F;1003-1002/Product: core protein P2-B *status predicted F;1003-1099/Product: core protein P2-B *status predicted F;1003-1099/Product: core protein P2-B *status predicted F;1100-1429/Product: core protein P2-A *status predicted F;1100-1429/Product: core protein P2-A *status predicted F;1100-1429/Product: core protein P3-A *status P3-A *status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: AF011368; NID: 92618824; PIDN: AAB84386.1; PID: 92618825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable thyroid receptor interactor - human (fragment)
NiAlternate names: CEV14 protein
C;Species: Homo sapiens (man)
C;Date: 24 Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C;Accession: T03719
C;Accession: N: Tanimoto, M:: Terasaki, H:: Marunouchi, T:: Saito, H.
Blood 90, 4271-4277, 1997
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Jun-2000
C;Accession: T21809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;1517/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted
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A;Molecule type: mRNA
A;Residues: 1-761 <ABE>
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Pred. No. 68;
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                                                                                         polyprotein - human rhinovirus 14
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illarity 41.2%;
Conservative
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Best Local Similarity 41.2%;
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Best Local 5
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                                                                                                                                                                                                                                                                                ATP Synthase, chain A TCO582 [imported] - Chlamydia muridarum (strain Nigg)
C; Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C; Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C; Species: B1687
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A; Reference number: A81500; MUID:20150255; PMID:10684935
A; Accession: E81687
A; Retus: preliminary
A; Molecule type: DNA
A; Residues: 1-591
A; Cross-references: GB:AE002326; GB:AE002160; NID:97190614; PIDN:AAF39416.1; PID:9719062
A; Genetics:
A; Genetics:
A; Gene: TCO582
C; Superfamily: vacuolar H+-transporting ATP synthase alpha chain homology <ATP>
F; 265-445/Domain: H+-transporting ATP synthase alpha chain homology <ATP>
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58;
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                                                          Score 55;
Pred. No. 5
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53.8%;
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nes 10; Conservative
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Best Local S:
Matches 10
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Wed Apr 16

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Profess Table [imported] - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Accession: F87908 | E87908 | E87908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 1
A;Introns: 45/1; 282/2; 312/3; 416/2; 1255/3; 1329/3; 1418/3; 1776/2; 1988/2; 2760/2
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-lik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein T22A3.8 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Sacession: T23064; T25096
R;Barlow, K.
submitted to the EMBL Data Library, October 1997
A;Reference number: 219669
A;Reference number: 219669
A;Residues: 1-2823 <WILL>
A;Cross-references: EMBL:AL008585; PIDN:CAA15432.1; GSPDB:GN00019; CESP:T22A3.8
A;Experimental source: clone H10E24
A;McMurray, A.
Submitted to the EMBL Data Library, October 1996
A;Reference number: 219980
A;Reference number: 219980
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T25096
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: EMBL:281125; PIDN:CAB03385.1; GSPDB:GN00019; CESP:T22A3.8
A;Cross-references: EMBL:281125; PIDN:CAB03385.1; GSPDB:GN00019; CESP:T22A3.8
A;Cross-references: EMBL:28125A3.8
                                A;Molecule type: DNA
A;Residues: 1.1957 <CON>
A;Residues: 1.1957 <CON>
A;Cross-references: EMBL:Z70690; PIDN:CAA94624.1; GSPDB:GN00066; SPDB:SPAC1F3.06c
A;Experimental source: strain 972h-; cosmid c1F3
C;Genetics:
A;Gene: SPDB:SPAC1F3.06c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN:CAA15432.1; GSPDB:GN00019; CESP:T22A3.8
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Pred. No. 2.7e+02;
5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                              Ouery Match 31.6%; Score 54; DB 2; Ler
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 6; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1394 KLKNQLDHLNQEIRLKEDVLKEKESL 1419
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55.6%;
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1874 LNETIFEDLKNRIDVLEQ 1891
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Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: CESP:T22A3.8
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R;Chui, C.
submitted to the EMBL Data Library, October 1994
A;Reference number: 219473
A;Reference number: 219473
A;Reference number: 219473
A;Accession: T21809
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: DNA
A;Residues: 1-1549
A;Cross-references: EMBL: 246242; PIDN: CAA86336.1; GSPDB: GN00021; CESP: F35G12.8
A;Cross-references: clone F35G12
C;Genetics:
A;Gene: CESP: F35G12.8
A;Introns: 50/3; 72/3; 177/3; 235/3; 333/2; 581/3; 667/3; 812/3; 882/1; 1050/3; 1223/3;
C;Superfamily: chromosome segregation protein SMC1
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A;Introns: 65/3; 101/3; 194/3; 269/3; 299/2; 373/3; 481/3; 576/3; 615/2; 704/3; 839/1;
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submitted to the EMBL Data Library, March 1997
A; Reference number: 219872
A; Accession: T24305
A; Stetus: prealininary; translated from GB/EMBL/DDBJ
A; Wolecule type: DNA
A; Residues: 1-1893 < W12>
A; Residues: 1-1893 < W12>
A; Experimental source: clone T01G1
A; Experimental source: clone T01G1
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A;Experimental source: clone F54E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appothetical protein T01G1.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T22661, T24305
R;White, S.; Mortimore, B.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19594
A;Reference number: Z19594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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A;Reference number: 221767
A;Accession: T38077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54; DB 2; Length 154
Pred. No. 1.5e+02;
6; Mismatches 8; Indels
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A;Molecule type: DNA
A;Residues: 1-1893 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |: |||: : | :| |: || || 874 KIVEELEKKRDELGEEAAKVKARQA 898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.6%;
44.0%;
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Best Local Similarity 44.0°
Matches 11; Conservative
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les 15; Conserv
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A; Accession: E87908
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-2823 < 8572>
A; Cross-references: GB:chr_I; PIDN:CAB03385.1; PID:g3924881; GSPDB:GN00019; CESP:T22A3.8
C; Genetics:
A; Genetics:
A; Map position: 1
C; Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h
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Db 1874 LNETIFEDLKNRIDVLEQ 1891
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April 15, 2003, 11:48:39 ; Search time 23.25 Seconds (without alignments) 241.276 Million cell updates/sec
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GenCore version 5.1.4_-p5_-4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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171
1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK
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                                                                                                                                                                                                                                                                                                                                                                   704857 seqs, 155824263 residues
                                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Database

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
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6: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Appl		Appl	Appl	Appli	Appl	Appl	Appl	Appl	Appl	1559, Ap	Appl	Appl	Appli	Appl	Appli	Appl	Appl	Appl	Appl	Appl.	Appl	Appl	Ap	Appl	Appl
ë	37.	36,	71,	27,	7, 1	25,	13,	62,	62,	62,	155	24,	35,	2,	28,	. '9	26,	29,	31,	32,	33,	34,	39,	4347	38,	55,
Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sednence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
	 - -																									
DB ID	5 US-09-445-576A-37	5 US-09-445-576A-36	5 US-09-445-576A-71	5 US-09-445-576A-27	5 US-09-445-576A-7	5 US-09-445-576A-25	1 PCT-US02-38407-13	5 US-09-992-095B-62	5 US-09-999-570-62	6 US-10-154-678-62	6 US-10-276-781-1559	5 US-09-445-576A-24	5 US-09-445-576A-35	5 US-09-445-576A-5	5 US-09-445-576A-28	5 US-09-445-576A-6	5 US-09-445-576A-26	5 US-09-445-576A-29	5 US-09-445-576A-31	5 US-09-445-576A-32	5 US-09-445-576A-33	5 US-09-445-576A-34	5 US-09-445-576A-39	5 US-09-513-999C-4342	5 US-09-445-576A-38	1 PCT-US02-19669A-55
Length DB	36	36	25	180	181	197	202	202	202	202	202	228	21	25	73	49	9	69	145	330	331	592	36	29	36	197
Query Match I	100.0	85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	85.4	82.5	79.5	79.5	74.9	74.9	72.5	72.5	72.5	72.5	72.5	52.0	48.0	44.4	42.1
Score	171	146	146	146	146	146	146	146	146	146	146	146	141	136	136	128	128	124	124	124	124	124	83	82	97	72
Result No.	7	7	3	4	5	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56

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Gaps

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Length 36; Indels

Query Match 85.4%; Score 146; DB 5; I Best Local Similarity 80.6%; Pred. No. 1.1e-14; Matches 29; Conservative 6; Mismatches 1;

ORGANISM: Homo sapiens

SEQ ID NO 36 LENGTH: 36 TYPE: PRT

US-09-445-576A-36

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Sequence 57, Appl Sequence 403, App Sequence 276, App Sequence 40, Appl Sequence 40, Appl Sequence 45353, A Sequence 8627, Ap Sequence 64349, A Sequence 54349, A Sequence 54349, A Sequence 2168, A Sequence 2168, A Sequence 2168, A Sequence 2168, A		Length 36; Indels 0; Gaps 0;
1 PCT-US02-19669A-57 5 US-09-989-733-403 5 US-09-992-643-403 6 US-10-125-933A-276 6 US-10-125-923A-276 6 US-10-174-575-276 6 US-10-174-575-276 6 US-10-187-75-276 6 US-10-199-672-276 6 US-10-199-672-276 6 US-10-199-672-276 7 US-60-445-576A-45353 7 US-60-453-135-8627 6 US-10-282-122A-54349 6 US-10-282-122A-54349 6 US-10-282-122A-7168 6 US-10-282-122A-7168 6 US-10-282-122A-7168 6 US-10-282-122A-7168	ALIGNMENTS US/09445576A. A/S erising module erising module 10004 100-07-17 4. on 3.1	DB 5; 2.5e-18; es 0; K 36 K 36
27 72 42.1 206 28 72 42.1 206 30 72 42.1 206 31 72 42.1 206 33 72 42.1 206 34 72 42.1 206 35 72 42.1 206 36 72 42.1 206 37 72 42.1 206 36 72 42.1 206 37 72 42.1 206 38 64 42.1 206 39 59 34.5 37.4 370 41 56 32.7 669 42 55 32.2 1178 44 54.5 31.9 519	RESULT 1 US-09-445-576A-37 Sequence 37, Application US/09445576A. Sequence 37, Application US/09445576A. FULLE OF INVENTION: Trimerising modul: FILE PREPERBONCE: 62032.000004 CURRENT ELILMG DATE: 2000-07-17 NUMBER OF SEQ ID NOS: 104. SOFTWARE: PATENTIN OFFIX. SOFTWARE: PATENTIN OFFIX. LENGTH: 36 TYPE: PRT CREATH: 36 TYPE: PRT US-09-445-576A-37	Query Match Best Local Similarity Matches 36; Conservat Matches 36; Conservat

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OTHER INFORMATION: Mature tetranectin single chain
              ; OTHER INFO
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ORGANISM:
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Pred. No. 1.8e-14;
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Pred. No. 9e-14;
6; Mismatches 1
 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                   1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
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                                                                                                     APPLICANT: Borean Pharma A/S
TILE OF INVENTION: Trimerising module
FILE REFERENCE: 62032.000004
CURRENT APPLICATION NUMBER: US/09/445,576A
CURRENT APPLICATION NUMBER: US/09/445,576A
SOFTWARE: Patentin version 3.1
SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Borean Pharma A/S
TILE OF INVENTION: Trimerising module
FILE REFERENCE: 62032 000004
CURRENT PELLING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.1
LENGTH: 180
                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Trimerising module
FILE REFERENCE: 62032.000004
CURRENT APPLICATION NUMBER: US/09/445,576A
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PATENTIN VERSION 3.1
                                                                          Sequence 71, Application US/09445576A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                            85.4%;
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US-09-445-576A-27
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.6
Matches 29; Conservative
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Best Local Similarity 80.6
Matches 29; Conservative
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; ORGANISM: Homo sapiens
US-09-445-576A-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial
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ORGANISM: Artificial
                                           RESULT 3
US-09-445-576A-71
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LENGTH: 181
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APPLICANT: BRISCOL-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE DEVELOPME
TITLE OF INVENTION: OSTEOARTHRITIS
TITLE OF INVENTION: OSTEOARTHRITIS
TITLE OF ILINGNIAN : OSTEOARTHRITIS
TITLE OF ILINGNIAN : OSTEOARTHRITIS
CURRENT APPLICATION NUMBER: PCT/USO2/38407
CURRENT FILING DATE: 2002-12-03
PRIOR FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 36
SOFTMARE: PatentIn version 3.1
LENGTH: 202
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         Length 181;
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   Score 146; DB 5;
Pred. No. 9e-14;
6; Mismatches 1
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Pred. No. 1e-13;
5; Mismatches
                                                                           1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
                                                                                                    17 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 52
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Pred. No. 1e-13;
6; Mismatches
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TITLE OF INVENTION: Trimerising module
FILE REFERENCE: 62032.000004
CURRENT APPLICATION NUMBER: US/09/445,576A
CURRENT FILING DATE: 2000-07-17
                                                                                                                                                                   RESULT 6
US-09-445-576A-25
; Sequence 25, Application US/09445576A
; GENERAL INFORMATION:
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US-09-992-095B-62
; Sequence 62, Application US/09992095B
; GENERAL INFORMATION:
     85.4%;
80.6%;
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SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 197
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80.6%;
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80.68;
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US-09-445-576A-25
Query Match
Best Local Similarity 80.68
Matches 29; Conservative
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Best Local Similarity 80.6
Matches 29; Conservative
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Best Local Similarity 80.6
Matches 29; Conservative
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PCT-US02-38407-13
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Gaps
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          Gaps
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TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 182 USI.REG
CURRENT TILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR PLING DATE: 2001-07-13
PRIOR PLING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR PLING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR PLING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
SPRIOR FILING DATE: 2001-06-15
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APPLICANT: Tang et al.
TTLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 2127-2018 (785 contig)
CURRENT APPLICATION NUMBER: US/10/276,781
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 2018
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1e-13;
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Pred. No. 1e-13;
                                                         1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
                                                                                     38 VVNTKMFEELKSRLDTLAQEVALLKEQOALOTVCLK 73
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Best Local Similarity 80.6%;
Matches 29; Conservative 6
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     Conservative
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; ORGANISM: Homo sapiens
US-10-276-781-1559
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 29; Conserva
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LOCATION: -21..-1
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US-10-154-678-62
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     29;
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     Matches
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        APPLICANT: Tanaka, HITCOAKI

TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US5.DIV
CURRENT APPLICATION NUMBER: US/09/992,095B
CURRENT FILING DATE: 2003-02-20
PRIOR PILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-06-15
PRIOR PAPLICATION NUMBER: US 60/302,277
PRIOR PLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
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TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 6-0910SOBDIV
CURRENT APPLICATION NUMBER: US/09/999,570
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR APPLICATION NUMBER: US 00/05,456
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR PELING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: US 60/293,574
PRIOR FILING DATE: US 60/293,574
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Pred. No. 1e-13;
6; Mismatches
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Pred. No. 1e-13;
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80.6%;
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ilarity 80.6%;
Conservative
APPLICANT: Benjanin, Stephane
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SOFTWARE: JPatent
SEQ ID NO 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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Best Local Similarity
Matches 29; Conserv
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US-09-992-095B-62
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US-09-999-570-62
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Length 52;

Score 136; DB 5; 1 Pred. No. 5.3e-13; 6; Mismatches 2;

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; OTHER INFORMATION: tetranectin polypeptide sequence for Glul to Lys52 US-09-445-576A-5
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TITLE OF INVENTION: Trimerising module
FILE REFERENCE: 62032.000004
CURRENT APPLICATION NUMBER: US/09/445,576A
CURRENT FILL GDATE: 2000-07-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PATCHILIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: April 15, 2003, 12:05:47 Job time: 23.25 secs
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Best Local Similarity 77.8%;
Matches 28; Conservative
                                                               Query Match 79.5%;
Best Local Similarity 77.8%;
Matches 28; Conservative
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US-09-445-576A-28
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LENGTH: 73
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Pred. No. 9.6e-14;
6; Mismatches 1.
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Pred. No. 1.2e-13;
6; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 VVNTKMFEELKSRLDTLAQEVALLKEQOALQTVCLK 99
38 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 73
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; GENERAL INFORMATION:

; APPLICANT: BOCTOR APPLICATION OF TABLE APPLICANT: BOCTOR APPLICATION TAINER APPLICATION UNMER: US/09/445,576A

; CURRENT APPLICATION NUMBER: US/09/445,576A

; CURRENT FILING DATE: 2000-07-17

; NUMBER OF SEQ ID NOS: 104

; SOFTWARE: PatentIn version 3.1
                                                                                                                                                APPLICANT: Borean Pharma A/S
TITLE OF INVEWTION: Trimerising module
FILE REFERENCE: 62032.000004
CURRENT APPLICATION NUMBER: US/09/445,576A
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Borean Pharma A/S
TITLE OF INVENTION: Trimerising module
FILE REFERENCE: 62032.000004
CURRENT APPLICATION NUMBER: US/09/445,576A
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.1
                                                               RESULT 12
US-09-445-576A-24
Sequence 24, Application US/09445576A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-09-445-576A-35
Geguence 35, Application US/09445576A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: CIIH6FXTN123
US-09-445-576A-24
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80.0%;
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Best Local Similarity 80.6%;
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-445-576A-35
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Best Local Similarity
Matches 28; Conserv
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LENGTH: 52
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LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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Gaps

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Length 73; Indels

Score 136; DB 5; I Pred. No. 8.3e-13; 6; Mismatches 2;

25, App 41342,

62, Appl 62, Appl 62, Appl 79, Appl 850, App 8650, App 8850, App 8850, Appl 12, Appl 13, Appl 13, Appl 13, Appl 13, Appl 13, Appl 13, Appl 14, Appl 16, Appl 17, Appl 10, Appl 11, Appl

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Sequence:

Minimum DB Maximum DB

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Searched:

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US-60-197-873-13425

US-09-445-576-27

US-09-445-576-27

US-09-245-576-25

US-09-924-340-62

US-09-934-340-62

US-09-934-360-62

US-10-000-886-62

US-10-000-886-62

US-10-000-886-62

US-10-238-659-667

US-10-238-659-667

US-10-238-659-667

US-09-445-576-24

US-09-987-107-12

US-09-987-107-3

US-09-987-107-3
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Pred. No. 3.6e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thogersen, Hans Christian
APPLICANT: Etzerodt, Michael
APPLICANT: Etzerodt, Michael
APPLICANT: Holtet, Thor Las
APPLICANT: Graversen, Niels Jonas Heilskov
APPLICANT: Kastrup, Jette Sandholm
APPLICANT: Nielsen, Bettina Bryde
APPLICANT: Nielsen, Bettina Bryde
APPLICANT: Nielsen, Bettina Bryde
APPLICANT: Larsen, Ingrid Kjoller
TITLE OF INVENTION: Trimerising module
FILE REFERENCE: THOGERSEN =1
CURRENT APPLICATION NUMBER: DC7/DK98/00245
PRIOR FILING DATE: 1998-06-11
PRIOR FILING DATE: 1998-06-11
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-445-576-36; Sequence 36, Application US/09445576; GENERAL INFORMATION:
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100.0%;
Query Match
Best Local Similarity
                                                                                                                                                                                                                                               ; ORGANISM: Murine US-09-445-576-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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 Sequence 36, Appl
Sequence 40, Appl
Sequence 28929, A
Sequence 40295, A
Sequence 35, Appl
Sequence 39, Appl
                                                                                                 April 15, 2003, 11:48:05 ; Search time 183 Seconds (without alignments) 126.833 Million cell updates/sec
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| cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
| cgn2_6/ptodata/1/paa/USO6_COMB.pep:*
| cgn2_6/ptodata/1/paa/USO6_COMB.pep:*
| cgn2_6/ptodata/1/paa/USO8_COMB.pep:*
| cgn2_6/ptodata/1/paa/USO9_COMB.pep:*
            GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                              1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
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US-09-987-107-40
US-09-791-537-28929
US-09-791-537-40295
US-09-445-576-35
US-09-987-107-39
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                                                                                                                                                                                                                                                                          4569144 seqs, 644733110 residues
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Listing first 45 summaries
                                                                         protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Perfect score:
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171
171
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146
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sequence

Length 36;

Result

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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PALENTIN VERSION 3.0
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Best Local Similarity 100.0%; Pred. No. 3.4e-15;
Matches 36; Conservative 0; Mismatches 0;
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Pred. No. 1.1e-12;
6; Mismatches 1
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GERREAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
TITLE OF INVENTION: APPLICANT:
FILE OF INVENTION: APPLILOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT APPLICATION NUMBER: US/09/987,107
PRIOR RAPPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
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GENERAL INFORMATION:
APPLICANT: Thogersen, Hans Christian
APPLICANT: Etzerodt, Michael
APPLICANT: Etzerodt, Michael
APPLICANT: Graversen, Naichael
APPLICANT: Graversen, Niels Jonas Heilskov
APPLICANT: Mastrup, Jette Sandholm
APPLICANT: Mastrup, Jette Sandholm
APPLICANT: Mastrup, Jette Sandholm
APPLICANT: Mielsen, Bettina Bryde
APPLICANT: Nielsen, Betting module
FILE REFERENCE: THOGERSEN -1
CURRENT FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: DK 7089/00245
PRIOR PLING DATE: 1998-06-11
PRIOR FILING DATE: 1998-06-11
PRIOR FILING DATE: 1998-06-11
PRIOR FILING DATE: 1997-06-11
SEQ ID NO 35
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 85.4%;
Best Local Similarity 80.6%;
Matches 29; Conservative
                       APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                       ; ORGANISM: Mus musculus
US-09-791-537-40295
                                               Debe, Derek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-445-576-35
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US-09-987-107-39
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Bonomix, Inc.
APPLICANT: Danser, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEQ ID NO 25929
LENGTH: 202
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             Indels
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0
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3.6e-16;
thes 0;
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100.0%; Pred. No. 3.4e-15;
Live 0; Mismatches 0;
                                                                                                                                                                              Sequence 40, Application US/09987107
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MOESTRUP, SOCIEN
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
FRIOR FILING DATE: 2001-01-26
FRIOR FILING DATE: 2001-01-15
FRIOR APPLICATION NUMBER: DK PA2001 00057
FRIOR APPLICATION NUMBER: DK PA2001 00057
FRIOR APPLICATION NUMBER: DK PA2001 00057
FRIOR FILING DATE: 2001-01-15
FRIOR FILING DATE: 2001-11-10
SOFTWARE: PATENT VERSION 3.1
SEQ ID NO 40
FRIOR FILING DATE: 2000-11-10
SOFTWARE: PATENT VERSION 3.1
SEQ ID NO 40
FRIOR PATENT VERSION 3.1
                                     1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
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100.0%; Score 171;
Best Local Similarity 100.0%; Pred. No. 3
Matches 36; Conservative 0; Mismatche
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Sequence 40295, Application US/09791537

GENERAL INFORMATION:
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  Conservative
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Best Local Similarity 100.
Matches 36; Conservative
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; ORGANISM: Mus musculus
US-09-987-107-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mus musculus
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36;
Matches
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; OTHER INFORMATION: Description of Artificial Sequence:H6FXTN23
US-09-445-576-27
                                                                                                                                                   85.4%; Score 146; DB 27;
80.6%; Pred. No. 3.9e-12;
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Pred. No. 9e-12;
                                                                                                                                                                                                                                        1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
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                                                                                                                                                                                             6; Mismatches
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APPLICANT: Holtet, Thor Las
APPLICANT: Graversen, Niels Jonas Heilskov
APPLICANT: Kastrup, Jette Sandholm
APPLICANT: Nielsen, Bettina Bryde
APPLICANT: Larsen, Ingrid Kjoller
TITLE OF INVENTION: Trimerising module
FILE REFERENCE: THOGERSEN =1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Etzerodt, Michael
APPLICANT: Holtet, Thor Las
APPLICANT: Graversen, Niels Jonas Heilskov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/445,576
CURRENT FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: PCT/DK98/00245
PRIOR FILING DATE: 1998-06-11
PRIOR FILING DATE: 1997-06-11
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APPLICANT: Nielsen, Bettina Bryde
APPLICANT: Larsen, Ingrid Kjoller
TITLE OF INVENTION: Trimerising module
FILE REFERENCE: THOGERSEN =1
CURRENT APPLICATION NUMBER: US/09/445,576
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PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: DK 0685/97
PRIOR FILING DATE: 1997-06-11
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                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Thogersen, Hans Christian
APPLICANT: Etzerodt, Michael
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/09445576 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 7, Application US/09445576 ; GENERAL INFORMATION:
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Best Local Similarity 80.6%;
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                             Conservative
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                        ORGANISM: Homo sapiens
                                                                                                                                                                     Best Local Similarity
Matches 29; Conserv
                                                                                       ; LOCATION: -21..-1
US-60-197-873-13425
                                            FEATURE:
NAME/KEY: SIGNAL
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Pred. No. 1.1e-12;
6; Mismatches 1; Indels
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GENERAL INFORMATION:
APPLICANT: Bejanin, Stc;hane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Jobart, Severin
APPLICANT: Glordano, Jean-Yves
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.US1.PRO
CURRENT APPLICATION NUMBER: US/60/197,873
CURRENT FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
APPLICANT: Tanaka, Hiroaki
APPLICANT: Johert, Severin
APPLICANT: Johert, Severin
APPLICANT: Giordano, Jaan-Yves
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.US2.REG
CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT FILING DATE: 2001-04-13
PRIOR PRILING DATE: 2000-04-18
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Pred. No. 3.9e-12;
6; Mismatches 1;
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PRIOR APPLICATION NUMBER: DK PA2001 00057 PRIOR FILING DATE: 2001-01-15
                                        APPLICATION NUMBER: DK PA2000 01682
                                   PRIOR APPLICATION NUMBER: DK PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin version 3.1
SEQ ID NO 39
LENGTH: 36
                                                                                                                                                                                                                                                          85.4%;
80.6%;
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80.6%;
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SOFTWARE: Patent.pm
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Best Local Similarity 80.6
Matches 29; Conservative
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                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-987-107-39
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ORGANISM: Homo sapiens
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Matches 29; Conserv
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; LOCATION: -21...1
US-09-834-366-13425
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LENGTH: 95
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LENGTH: 95
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Length 180;

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APPLICANT: Tanaka, Hiroaki
TTLEOF TTLEOF THORN THOMN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.052.REG
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
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TITLE OF INVENTION: SUCHIOLINE
FILE REFERENCE: 91.034.DIV
CURRENT APPLICATION HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.034.DIV
CURRENT APPLICATION NUMBER: US/09/924,340
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR APPLICATION NUMBER: US 60/293,574
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                                                          85.4%; Score 146; DB 21; Length 202; 80.6%; Pred. No. 1e-11; 1.1ve 6; Mismatches 1; Indels (
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Pred. No. 1e-11;
6; Mismatches
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                                                                                                                                                                                                                                                                                                                  US-09-924-340-62; Sequence 62, Application US/09924340; GENERAL INFORMATION:
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Best Local Similarity 80.6%;
Matches 29; Conservative
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                                                                                                               Conservative
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SOFTWARE: JPatent
SEQ ID NO 62
LENGTH: 202
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NUMBER OF SEQ ID NOS: 114
SOFTWARE: JPatent
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                                                          Query Match
Best Local Similarity
Matches 29; Conserv
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          US-09-791-537-41342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: 1..21
US-09-924-340-62
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GERERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Joseph
TITLE OF INVENTION: WETHORS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICANTON STORY OF USE THEREOF
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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US-09-445-576-25
                                                                                                                                                                                                            Length 181;
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Pred. No. 9.1e-12;
6; Mismatches 1;
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APPLICANT: Graversen, Niels Jonas Heilskov
APPLICANT: Graversen, Niels Jonas Heilskov
APPLICANT: Rastrup, Jette Sandholm
APPLICANT: Larsen, Ingrid Kjoller
TITLE OF INVENTION: Trimerising module
FILE REFERENCE: THOGENSEN = 1009/445,576
CURRENT APPLICATION NUMBER: US/09/445,576
CURRENT FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: DKT/DK98/00245
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1008-06-11
NUMBER OF SEQ ID NOS: 60
SOFTAME: PATENT VOE: 2.0
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APPLICANT: Etzerodt, Michael
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                                                                                                                                                                                                            85.4%;
80.6%;
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NUMBER OF SEQ ID NOS: 60 SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 80.6
Matches 29; Conservative
                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-791-537-41342
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LENGTH: 202
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| Sequence 62, Application US/09994590
| GENERAL INFORMATION: Stephane
| APPLICANT: Benjamin, Stephane
| APPLICANT: Tanaka, Hiroaki
| TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
| FILE REFERENCE: 91.033.DIV
| CURRENT APPLICATION NUMBER: US/09/994,590
| CURRENT FILING DATE: 2001-11-13
| PRIOR APPLICATION NUMBER: US 09/924,340
| PRIOR FILING DATE: 2001-08-06
| PRIOR APPLICATION NUMBER: US 60/305,456
| PRIOR APPLICATION NUMBER: US 60/305,456
| PRIOR FILING DATE: 2001-07-13
| PRIOR FILING DATE: 2001-06-19
| PRIOR FILING DATE: 2001-06-15
| PRIOR FILING DATE: 2001-06-25
| PRIOR FILING DATE: 2001-06-25
| NUMBER OF SEQ ID NOS: 112
| SEQ ID NO 62
| LUBGTH: 202
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85.4%; Score 146; DB 23; Length 202;
Best Local Similarity 80.6%; Pred. No. 1e-11;
Matches 29; Conservative 6; Mismatches 1; Indels
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Pred. No. 1e-11;
6; Mismatches 1; Indels
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80.6%;
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Best Local Similarity 80.6
Matches 29; Conservative
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CRGNISM: Homo sapiens

FATURE:

NAME/KEY: SIGNAL

LOCATION: 1..21

US-09-994-590-62
; SEQ ID NO 62
: LENGTH: 202
; TYPE: PRT
: ORGANISM: Homo sapiens
; FEATURE:
                                                                                           ; NAME/KEY: SIGNAL
; LOCATION: 1..21
US-09-992-600A-62
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US-09-994-590-62
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Search completed: April 15, 2003, 12:04:07 Job time : 183 secs

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GenCore version 5.1.4_p5_4578

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OM protein - protein search, using sw model

Run on: April 15, 2003, 11:50:25; Search time 10 Seconds

(without alignments)
220.090 Million cell updates/sec

Title:

US-09-445-576A-37

Perfect score: 171
Sequence: 1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36 in Gapop 10.0, Gapext 0.5

Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0

Maximum DB seq length: 2000000000
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Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USOG_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Appl	Appl	Appl	App1	Appl	Appl	Appli	Appl	Appli	Appli	Appli	Appli	Appli	Appli	Appl	Appl	Appl	Appl	Appl
	u	40,	39,	62,	62,	12,	13,	4	50,	ς,	5,	9	7,	8	6	10,	11,	48,	54,	56,
	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 4	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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	ID	US-09-987-107-40	US-09-987-107-39	US-09-924-340-62	US-09-992-600A-62	US-09-987-107-12	US-09-987-107-13	US-09-987-107-4	US-09-987-107-50	US-09-987-107-3	US-09-987-107-5	US-09-987-107-6	US-09-987-107-7	US-09-987-107-8	US-09-987-107-9	US-09-987-107-10	US-09-987-107-11	US-09-987-107-48	US-09-987-107-54	US-09-987-107-56
	DB	6	σ	6	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ	σ	6	δ	δ	σ
	Query Match Length DB	36	36	202	202	51	58	258	273	301	301	304	304	304	306	306	306	316	316	323
æ	Query Match	100.0	85.4	85.4	85.4	82.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5
	Score	171	146	146	146	141	136	136	136	136	136	136	136	136	136	136	136	136	136	136
	Result No.	1	7	m	4	S	9	7	ω	6	10	11	12	13	14	15	16	17	18	19

Sequence 58, Appl Sequence 60, Appl Sequence 64, Appl Sequence 64, Appl Sequence 64, Appl Sequence 42, Appl Sequence 99, Appl Sequence 91, Appl Sequence 10, Appl Sequence 403, Appl Sequence 23, Appl Sequence 23, Appl Sequence 24, Appl Sequence 276, Appl Sequen		Length 36; Indels 0; Gaps 0;
US-09-987-107-58 US-09-987-107-60 US-09-987-107-62 US-09-987-107-64 US-09-987-107-64 US-09-987-107-42 US-09-987-107-42 US-09-987-107-41 US-09-981-107-41 US-09-991-2934-403 US-09-991-293-687-403 US-09-991-294-403 US-09-991-294-403 US-09-991-294-403 US-09-991-294-403 US-09-991-294-403 US-09-991-294-403 US-09-991-294-403 US-09-991-294-403 US-09-991-294-403 US-09-991-274-403	ALIGNMENTS 1 cation US/09987107 20.1 20	171; DB 9; No. 2.6e-16; matches 0; OTVCLK 36 OTVCLK 36
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2000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	-40 US20020156007a1 US20020156007a1 CRAVERSEN, JONA GRAVERSEN, JONA MOESTRUP, SOFA INVENTION: APOLIP PELICATION NUMBER: LING DATE: 2001-01 LICATION NUMBER: LING DATE: 2001-01 SEQ ID NOS: 91 SEQ ID NOS: 91 SEQ ID NOS: 91 SEQ ID NOS: 91 OFA SEQ ID NOS: 91	ty 100 ervative NRMDVLAQI NRMDVLAQI NRMDVLAQI NRMDVLAQI UP, Sored APOLIPE
C C C C C C C C C C C C C C C C C C C	40 Applicatio SEAUSO02015600 SEAUSESEN, GRAVERSEN, WENTION: GRAVERSEN, WENTION: ARSKE: GRAVER LICATION NUMB GOTE: 200 CATION NUMB NG DATE: 200 CA	Similarity 36; Conserv SSKWPEELKNRM
1113333 11133333 113333333333333333333	-107-40 e 40. Ay NO. USZJ INFORM ANT: GR ANT: GR ANT: GR APLICA FILING APPLICA FILING APPLICA FILING APPLICA FILING APPLICA FILING APPLICA FILING APPLICA FILING H: 36 PH:	watch Local Sin hes 36; 1 LVSSKI 1 LVSSKI 1 2 Sept. 107-3; 987-107-3; At No. US; RAL INFORMIT: LICANT: LE OF INVY
222 222 222 222 222 223 233 233 244 244	RESULT 1 US-09-987-107-40 US-09-987-107-40 Sequence 40, Application US/09987107 PAPELICANT GRAVERSEN JONAS APPLICANT GRAVERSEN JONAS TITLE OF INVENTION: APOLIPOPROTEINS AN TITLE OF INVENTION: APOLIPOPROTEINS AN CURRENT APPLICATION NUMBER: US/09/987, CURRENT FILING DATE: 2001-11-13 PRIOR PPLICATION NUMBER: US 60/264, 02 PRIOR PRILOR DATE: 2001-01-26 PRIOR FILING DATE: 2001-01-15 PRIOR FILING DATE: 2001-01-15 PRIOR FILING DATE: 2001-11-15	Query Match Best Local Similarity 100.0%; Score Best Local Similarity 100.0%; Pred. Matches 36; Conservative 0; Miss Oy 1 LVSKMFEELKNRMDVLAQEVALLKEKQAL.
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Pred. No. 4e-12;
6; Mismatches 1;
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Pred. No. 3.7e-12;
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APPLICANT: GRAVERSEN, Jones
APPLICANT: MESTRUP, SCREEN
TITLE OF INVENTION: APPLICAPERING ANALOGUES
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-15
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                                         CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR PELLORICATION NUMBER: US 60/305,456
PRIOR PELLORICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-25
SEQ ID NO 62
LENGTHARE. JPATENT
LENGTHARE OF SEQ ID NOS: 114
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SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 51
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80.0%;
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80.6%;
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Best Local Similarity 80.65
Matches 29; Conservative
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Best Local Similarity 80.0
Matches 28; Conservative
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US-09-987-107-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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; LOCATION: 1..21
US-09-992-600A-62
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Sequence 62, Application US/09924340

Publication No. US20030027248A1

GENERAL INFORMATION:

APPLICANT: Bejanin, Stephane

APPLICANT: Tanaka, Hiroaki

TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91.US2.REC

CURRENT APPLICATION NUMBER: US 60/924,340

CURRENT FILING DATE: 2001-08-06

PRIOR PELING DATE: 2001-07-13

PRIOR PELING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/302,277

PRIOR APPLICATION NUMBER: US 60/298,698

PRIOR APPLICATION NUMBER: US 60/298,698

PRIOR PLING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

NUMBER OF SEQ ID NOS: 112

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Publication No. US20030027161A1
GENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.4%; Score 146; DB 9; Length 202; 80.6%; Pred. No. 4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 5.4e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
FRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR PILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
SPRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PATENTIN VETSION 3.1
SET OF THE PATENTIN VETSION 3.1
SET OF THE PATENTIN VETSION 3.1
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Best Local Similarity 80.6%;
Matches 29; Conservative
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Matches 29; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-987-107-39
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US-09-992-600A-62
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LENGTH: 202
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US-09-987-107-50
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OTHER INFORMATION: Trimerisation module from tetranectin NAME/KEY: misc_feature
LOCATION: (59)...(301)
77.8%; Pred. No. 1.1e-10; ative 6; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 79.5%; Score 136; DB 9; Best Local Similarity 77.8%; Pred. No. 1.2e-10; Matches 28; Conservative 6; Mismatches 2
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FILE REFERENCE: GRAVERSERIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 3
LENGTH: 301
                                                                                                                                                                                                                                                                                           APPLICANT: GRAVERSEN, Jonas
APPLICANT: GRAVERSEN, Jonas
APPLICANT: MCESTRUP, SOTEN
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REPERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/99/987,107
CURRENT APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PATCH IN VERSION 3.1
                                                                                          1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
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Patent No. US20020156007A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
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APPLICANT: GRAVERSEN, Jonas
APPLICANT: MOESTRUP, Soren
  Best Local Similarity 77.89
Matches 28; Conservative
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ORGANISM: Homo sapiens
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US-09-987-107-50
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US-09-987-107-3
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OTHER INFORMATION: Trimerisation module from tetranectin NAME/KEY: misc_feature
LOCATION: (59)..(258)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (59)..(258)
; OTHER INFORMATION: Amion acids 68-267 from human Apo Al
US-09-987-107-4
                          APPLICANT: GRAVERSEM, JOHNES
APPLICANT: MOESTRUP, SOTEEN
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: DK PA2001 00057
PRIOR FILING DATE: 2001-01-26
PRIOR FLILING DATE: 2001-01-15
SEQ ID NOS: 91
SEQ ID NO 13
LENGTH: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: APOLITODENCE IN TITLE OF INVENTION: APOLITODENCE IN COURENT APPLICATION NUMBER: US/09/987,107 CURRENT FILING DATE: 2001-11.13 PRIOR APPLICATION NUMBER: US 60/264,022 PRIOR FILING DATE: 2001-01-26 PRIOR FILING DATE: 2001-01-26 PRIOR FILING DATE: 2001-01-15 PRIOR FILING DATE: 2001-01-15 PRIOR FILING DATE: 2000-11-10 NUMBER: DK PAZONO 01682 PRIOR FILING DATE: 2001-01-15 PRIOR FILING DATE: 2000-11-10 NUMBER OF SEQ ID NOS: 91 SOFTWARE: PALENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 136; DB 9
Pred. No. 2e-11;
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LOCATION: (1)..(4)
OTHER INFORMATION: Linker sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09987107
Patent No. US20020156007A1
GENERAL INFORMATION:
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Best Local Similarity 77.8%;
Matches 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (57)...(58); OTHER INFORMATION: Linker US-09-987-107-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MOESTRUP
  GENERAL INFORMATION:
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US-09-987-107-4
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Query Match

FEATURE:

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Length 304;
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LOCATION: (1)..(58)
OTHER INFORMATION: Trimerisation module from tetranectin
NAME/KEY: misc_feature
LOCATION: (59)..(61)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.5%; Score 136; DB 9; 31 Tarity 77.8%; Pred. No. 1.4e-10; Conservative 6; Mismatches 2;
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Sequence 7, Application US/09987107
Sequence 7, Application US/09987107
Sequence 7, Application US/09987107
Sequence 7, Application US/09987107
SENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
APPLICANT: MOESTRUP, SOZEN
TILE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REFRENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT APPLICATION NUMBER: US 60/264,022
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR APPLICATION NUMBER: DX 60/264,022
PRIOR APPLICATION NUMBER: DX 60/264,022
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DX PA2000 01682
PRIOR APPLICATION NUMBER: DX PA2000 01682
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PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PATENTIN Version 3.1
SEQ ID NO 6
LENGTH: 304
                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Linker
NAME/KEY: misc_feature
CCATION: (62)..(304)
US-09-987-107-6
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
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                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 28; Conserv
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COTHER INFORMATION: Trimerisation module from tetranectin NAME/FER: misc_feature
LOCATION: (9)..(9)

OTHER INFORMATION: Mutagen
NAME/FER: misc_feature
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19.5%; Score 136; DB 9;
Best Local Similarity 77.8%; Pred. No. 1.3e-10;
Matches 28; Conservative 6; Mismatches 2.
                                                                                        Query Match 79.5%; Score 136; DB 9; Best Local Similarity 77.8%; Pred. No. 1.3e-10; Matches 28; Conservative 6; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09987107
Sequence 5, Application US/09987107
Fatent No. US20020156007a1
GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
APPLICANT: GRAVERSEN, Soren
TITLE OF INVENTION: APOLITOPROTEINS ANALOGUES
FILE PEEFRENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR FILING DATE: 2001-01-15
SEQ ID NO SEQ ID NOS: 91
SEQ ID NO SEQ ID NOS: 91
SEQ ID NO SEQ ID NOS: 91
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Fatent No. US20020156007A1
GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
TITLE OF INVENTION: APPLICANTION:
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION UNBERS. US/09/987,107
CURRENT FILING DATE: 2001-11-13
FRIOR PELIGNON NUMBER: US 60/264,022
FRIOR FILING DATE: 2001-01-26
FRIOR APPLICATION NUMBER: US 60/264,022
FRIOR FILING DATE: 2001-01-26
FRIOR APPLICATION NUMBER: US 60/264,022
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CHER INFORMATION: Mutagen
NAME/KEY: misc_feature
LOCATION: (59)..(301);
OTHER INFORMATION: Apo-Al mature
US-09-987-107-5
               ; OTHER INFORMATION: Mature ApoAl US-09-987-107-3
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US-09-987-107-5
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Gaps

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ö Gaps ; 0 Length 304; Query Match 79.5%; Score 136; DB 9; Length 30 Best Local Similarity 77.8%; Pred. No. 1.4e-10; Matches 28; Conservative 6; Mismatches 2; Indels COTHER INFORMATION: (1)..(56)
COTHER INFORMATION: Trimerisation module from tetranectin NAME/EEV: misc_feature
LOCATION: (57)..(61)
OTHER INFORMATION: Fibronectin based linker
NAME/EEV: misc_feature
LOCATION: (62)..(304)
COTHER INFORMATION: Mature Apo Al
US-09-987-107-7

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Gaps

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LOCATION: (1)..(58)
OTHER INFORMATION: Trimerisation module from tetranectin NAME/KEY: misc_feature
LOCATION: (59)..(63)
OTHER INFORMATION: Linker
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OTHER INFORMATION: Trimerisation module from tetranectin NAME/KEY: misc_feature
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Pred. No. 1.4e-10;
6; Mismatches 2
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77.8%; Pred. No. 1.4e-10;
Live 6; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITE OF INVENTION: APOLIPOPROTEINS ANALOGUES FILE REFERENCE: GRAVERSENIA CURRENT APPLICATION: APOLIPOPROTEINS ANALOGUES FILE REFERENCE: GRAVERSENIA CURRENT APPLICATION NUMBER: US/09/987,107 CURRENT FILING DATE: 2001-01-26 PRIOR PAPLICATION NUMBER: US 60/264,022 PRIOR FILING DATE: 2001-01-26 PRIOR FILING DATE: 2001-01-15 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-17 PRIOR FILING D
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OTHER INFORMATION: Tetranectin based linker NAME/KEX: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               completed: April 15, 2003, 12:06:35
ne : 11 secs
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; Sequence 10, Application US/09987107
; Patent No. US20020156007a1
; GENERAL INFORMATION:
                                                                                                                                                                     NAME/KEY: misc_feature
CCATION: (64)..(306)
CTHER INFORMATION: Mature Apo Al
US-09-987-107-9
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OTHER INFORMATION: Mature Apo Al
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Best Local Similarity 77.8%;
Matches 28; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GRAVERSEN, Jonas APPLICANT: MOESTRUP, Soren
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Best Local Similarity
Matches 28; Conserv
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LENGTH: 306
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Job time
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LOCATION: (1)..(56)
OTHER INFORMATION: Trimerisation module from tetranectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79.5%; Score 136; DB 9;
77.8%; Pred. No. 1.4e-10;
Live 6; Mismatches 2
                                                                                    Sequence 8, Application US/09987107
Sequence 8, Application US/09987107
Sequence 8, Application US/09987107
Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 9, TITLE APPLICANT: GRAVERSEN, Jonas APPLICANT: MOESTRUP, SOTEN
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES FILE OF ENERGY ENTER APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
SPRIOR FILING DATE: 2001-11-15
SOFTWARE: PALENTING NOWER: DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
SSEQ ID NO 89
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Patent No. US20020156007a1
GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
APPLICANT: GRAVERSEN, Jonas
APPLICANT: MOESTRUP, SOCIEN
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENA,
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
SOFTWARE: PARCHING PARE: 2001-01-15
SOFTWARE: PARCHIN VERSION 3.1
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OTHER INFORMATION: Mature Apo Al
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OTHER INFORMATION: Mutagen
NAME/KEY: misc_feature
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Best Local Similarity 77.89
Matches 28; Conservative
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OTHER INFORMATION: Mutagen
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LOCATION: (62)..(304)
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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                                                               US-09-987-107-8
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Best Local Similarity
STRANDEDNESS:
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105.923 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
                    GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-968-751-4
US-08-178-477B-29
US-08-178-477B-2
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5-08-469-658-56
5-09-602-877A-99
5-09-156-316-1
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-08-928-213B-8
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US-09-447-453-2
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-08-404-671-4
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US-09-724-517-2
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Maximum Match 100% '
Listing first 45 summaries
                                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Thosgersen, Hans Christian
APPLICANT: Holtet, Thor Las
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding of
TITLE OF INVENTION: proteins
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 146; DB 1;
Pred. No. 1.4e-13;
US-08-690-011A-19
US-08-692-254-2
US-08-645-900A-1
US-08-645-900A-1
US-08-223-8A-1
US-09-220-459-1
US-09-220-459-1
US-09-567-790A-1
US-09-567-790A-1
US-09-567-790A-1
US-09-567-790-1
US-09-567-790-1
US-09-567-790-1
US-08-256-790-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: OFFICE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version SOFTWARE: #1.25 #1.25 APPLICATION DATA: APPLICATION NUMBER: US/08/469,486
                                                                                                                                                                                                                                  US-08-410-540-2
                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFFERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEPAX: 617 542 8906
TELEX: 20016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: FEBRUARY 4, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                         Sequence 56, Application US/08469486 Patent No. 5739281 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Fish & Richardson
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 56:
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80.6%;
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LENGTH: 202 amino acids
TYPE: amino acid
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STREET: 220.
CITY: Boston
The: Massachusetts
  MOLECULE TYPE: protein
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REGISTRATION NUMBER:
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APPLICANT: Bernstein, Harold S.
APPLICANT: Coughlin, Shaun R.
TITLE OF INVENTION: Methods and Compositions for Regulating Cell Cycle
TITLE OF INVENTION: Progression
FILE REFERENCE: USF-020/010S
CURRENT APPLICATION NUMBER: US/09/156,316
CURRENT FILING DATE: 1998-09-18
EARLIER RELING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 12
        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                       Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.8%; Score 51; DB 4; Length 802; 52.6%; Pred. No. 34; Live 4; Mismatches 5; Indels
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APPLICANT: Stern, David M.
APPLICANT: Clauss, Matthias
APPLICANT: Kao, Janet
APPLICANT: Kao, Janet
APPLICANT: Kayton, Mark
APPLICANT: Libutti, Steven K.
APPLICANT: Libutti, Steven K.
TITLE OF INVENTION: Endothelial-Monocyte Activating
TITLE OF INVENTION: Polypeptide II: A Mediator Which
TITLE OF INVENTION: Activates Host Response
                                                                                                                                                                                                                                                                                     Score 72; DB 4;
Pred. No. 0.006;
5; Mismatches 7
                                            FILE REFERENCE: 210121.446C5
CURRENT APPLICATION NUMBER: US/09/602,877A
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 107
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
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; Patent No. 6183961
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Best Local Similarity 57.1%;
Matches 16; Conservative
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SEQ ID NO 1
LENGTH: 802
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Best Local Similarity 52.6
Matches 10; Conservative
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; ORGANISM: Homo sapiens
US-09-156-316-1
                                                                                                                                                                           ; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-602-877A-99
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US-08-129-456A-36
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US-09-156-316-1
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                                                                                                                                                                                    Sequence 56, Application US/08469658
Patent No. 5917018
GENERAL INFORMATION:
APPLICANT: The egersen, Hans Christian
APPLICANT: Holtet, Thor Las
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 58
      Indels
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80.6%; Pred. No. 1.4e-13;
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CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/469,658
FILING DATE: June 5, 1995
                                         1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
                                                                  38 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
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    6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFCATION 1530
PRIOR APPLICATION 1530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: FEBRUARY 4, 1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/00
TELECHOMUNICATION INFORMATION:
TELECHOME: 617 542 8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 99, Application US/09602877A Patent No. 6432707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 617 542 5070
TELEFRAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 202 amino acids
amino acid
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Xu, Jiangchun
Dillon, Davin C.
  Conservative
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Best Local Similarity 80.6
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-469-658-56
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02110-2804
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APPLICANT: Reed, Ste
APPLICANT: Xu, Jiang
APPLICANT: Dillon, I
                                                                                                                                                                                                                                                                                                                                                                                                            ALD...
STREET: ...
-mv: Boston
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                                                                                                                                               RESULT 2
US-08-469-658-56
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29;
  Matches
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Gaps

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Gaps
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                                                                                                         Length 310;
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                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bandman, Olga
APPLICANT: Coleman, Roger
APPLICANT: Coleman, Roger
APPLICANT: Au-Young, Janice
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
NUMBER OF SEQUENCES: 4
CORRESPENDIBNE ADDRESS:
ADDRESSE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                           DB 2;
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50; DB 3;
Pred. No. 15;
3; Mismatches
                                                                                                                                                Mismatches
                                                                                                           Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAMN: BILLINGS, LOUY J.
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0117 US
TELECOMMUNICATION INFORMATION:
TELEDHONE: 415-855-0555
TELEDHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOCTWARE: FRAKED VERSION 1.5
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,868
FILING DATE:
                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09123615
Patent No. 6090377
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.2%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                         29.2%;
61.1%;
                                                                                                                                                                                                     22 IEYLKQQVALLKEKAILQ 39
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Best Local Similarity 61.19
Matches 11; Conservative
                                                                                                         Query Match 29.2's
Best Local Similarity 61.1's
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                 IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 498910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: GenBank
CLONE: 498910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
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MOLECULE TYPE:
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                                                     ; CLONE: 4
US-08-705-868-3
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US-09-123-615-3
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APPLICANT: Coleman, Roger
APPLICANT: Au-Young, Janice
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0 Version #1.30
CURRENT APPLICATION DATA: US/08/129,456A
FILLING DATE: 29-SEP-1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50; DB J
Pred. No. 15;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0117·US
TELECOMUNICATION INFORMATION:
TELEPAX: 415-845-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,868
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41735
TELEPHONE: 212,278 0400
TELEPHONE: 212,278 0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08705868
Patent No. 5885798
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Coleman, Roger
                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.2%;
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                              LENGTH: 310 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-129-456A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 MDVLAQEVALLKEKQALQ 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: linear
             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            u.s.
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US-08-705-868-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY:
STATE:
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                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Reid, Robert A.
APPLICANT: Ackley, Rhonda L.
APPLICANT: Hemperly, John J.
TITLE OF INVENTION: HUMAN RESTRICTIN AND NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Richard J. Rodrick, Becton Dickinson and ADDRESSEE: Company STREET: 1 Becton Drive CITY: Franklin Lakes
                                                                                                          CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/08/928,213B
FILING DATE: 12-589-1997
CLASSIETCATION: CURNOWN
ATTORNEY/AGRNT IRFORMATION:
NAME: WASCAIGHT, AGMIN T.
REGISTRATION NUMBER: 38,230
TELECOMMUNICATION INFORMATION:
TELEFRENCE/DOCKET NUMBER: ENZYCO-02550
TELECOMMUNICATION INFORMATION:
TELEFRENCE/TOTAL 18705-8410
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-928-213B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 528 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
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; Patent No. 5591583
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ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Dona R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1358 amino acids
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Best Local Similarity
Matches 13; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 07417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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                                                                                   GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Stern, David M.
APPLICANT: Clauss, Matthias
APPLICANT: Kao, Janet
APPLICANT: Kayton, Mark
APPLICANT: Libuti, Steven K
APPLICANT: Libuti, Libuti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Seville, Mark
Cull, Millard G.
TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III
HOLOENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/360,821B
FILING DATE: 08-OCT-96
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ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
                                   Sequence 35, Application US/08360821B Patent No. 6228837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08928213B Patent No. 6238905 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.2%;
61.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 MDVLAQEVALLKEKQALQ 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 IEYLKQQVALLKEKAILQ 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 61.1
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: aminc sing
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 06 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10036
US-08-360-821B-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-360-821B-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-928-213B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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US-08-404-665-4

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Gaps
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                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rubinfeld, Bonnee
APPLICANT: Polakis, Paul G.
APPLICANT: Ligenfelter, Carol
APPLICANT: Vuong, Terilyn T.
TITLE OF INVENTION: MODULATORS OF BRCA1 ACTIVITY
CORRESPONDENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94806
ZIP: PAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: ONYX Pharmaceuticals, Inc.
STREET: 3031 Research Drive
CITY: Richmond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ONYX1024 GG
                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/968,75:
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|130 SAQVLQELLSRIEMLEREVSVLRDQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SSKMFEELKNRMDVLAQEVALLKEK 27
                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: FUGIT, Donna R.
REGISTRATION NUMBER: 32,135
REGISTRATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-968-751-4
; Sequence 4, Application US/08968751
; Patent No. 5948643
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Giotta, Gregory
REGISTRATION NUMBER: 32,028
REPERENCE/DOCKET NUMBER: ON
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (510) 262-8710
TELEFAX: (510) 222-9758
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1358 amino acids
3: Company
1 Becton Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                      Franklin Lakes
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                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Matches 8; Conserv
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                          COUNTRY:
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                                                        Gaps
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                                                        0;
                    DB 1; Length 1358;
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                                                        3; Indels
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APPLICANT: Reid, Robert A.
APPLICANT: Ackley, Rhonda L.
APPLICANT: Hemperly, John J.
TITLE OF INVENTION: HUMAN RESTRICTIN AND NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES
NUMBER OF SEQUENCES: 4
CORRESPONDENE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
                                                                                                                                                                                                                                                                              APPLICANT: Reid, Robert A.
APPLICANT: Reid, Rhonda L.
APPLICANT: Hemperly, Dhn J.
TITLE OF INVENTION: HUMAN RESTRICTIN AND NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES
NUMBER OF SEQUENCES:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
ADDRESSEE: Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.2%; Score 50; DB 32.0%; Pred. No. 88; tive 14; Mismatches
              Query Match

29.2%; Score 50; DB
Best Local Similarity 32.0%; Pred. No. 88;
Matches 8; Conservative 14; Mismatches
                                                                                                                3 SSKMFEELKNRMDVLAQEVALLKEK 27
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                                                                                                                                                                                    RESULT 11
US-08-404-671-4
; Sequence 4, Application US/08404671
; Patent No. 5635360
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-404-781-4; Sequence 4, Application US/08404781; Patent No. 5681931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1358 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Becton Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 29.2'
Best Local Similarity 32.0'
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: NJ
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Sequence 2, Application US/081784778
Patent No. 5756343
GENERAL INFORMATION:
GAPPLICANT: WU, CARL; CLOS, JOACHIM;
APPLICANT: WESTWOOD, J. TIMOTHY.; RABINDRAN, SRIDHAR TITLE OF INVENTION: CELL STRESS.
TITLE OF INVENTION: TRANSCRIPTIONAL FACTORS
                                                                                                                                                                                                                                                                                                                        COUNTY: USA

ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: WORDERFECT 5.1
SOFTWARE: WORDERFECT 5.1
APPLICATION NUMBER: US/08/178,477B
FILING DATE: Q'-JAN-1994
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 26-NOV-1990
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4103USI
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: April 15, 2003, 11:51:49 Job time : 11 secs
                                                                                                                                                                      NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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                                                                                                                                          DB 2; Length 835;
                                                                                                                                                                                         13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: WU, CARL; CLOS, JOACHIM;
APPLICANT: WESTWOOD, J., TIMOTHY.; RABINDRAN, SRIDHAR
TITLE OF INVENTION: CELL STRESS
TITLE OF INVENTION: TRANSCRIPTIONAL FACTORS
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                   ch 28.7%; Score 49; DB 3 Sinilarity 32.4%; Pred. No. 69; 11; Conservative 10; Mismatches
                                                                                                                                                                                                                                                            355 LENSRLATDLRAQLQILANMDSQLKELQSQHTHC 388
                                                                                                                                                                                                                           1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 5.5;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: WORDPERFECT 5.1
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/178,477B
FILING DATE: 07-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROCASSITION: 309
PROCASSITION: 309
PROCASSITION: 306
FILING DATE: 26-NOV-1990
CLASSIFICATION NUMBER: US/07/617,910
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4103US
TELECHONE: (212) 758-4800
TELEPRAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48;
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 29, Application US/08178477B Patent No. 5756343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: MONGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK COUNTRY: NEW YORK COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.1%;
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Best Local Similarity 40.0%
Matches 10; Conservative
LENGTH: 835 amino acids
                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELERA: (212) 751-684
TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                      Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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US-08-178-477B-29
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                                                                                                                                       Query Match
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                                                                                                                                                    Length 691;
                                                                                                                                                                          9; Indels
                                                                                                                                    76;
                                                                                                                                                Score 48; DB Pred. No. 76; 6; Mismatches
                                                                                                                                                                                                            7 FEELKNRMDVLAQEVALLKEKQALQ 31
   (212) 758-4800 (212) 751-6849
                                                                                                                                                28.1%;
40.0%;
TELEPHONE: (212) 758-481
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 691
                                                                                                                                             Query Match
Best Local Similarity 40.0
Matches 10; Conservative
                                                                                        SS: unknown unknown
                                                                                                           MOLECULE TYPE: protein
                                                                          amino acid
                                                                                STRANDEDNESS:
                                                                                                                       US-08-178-477B-2
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RESULT 15 US-08-178-477B-2

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April 15, 2003, 11:43:14 ; Search time 28.75 Seconds (without alignments) 166.853 Million cell updates/sec

Run on:

US-09-445-576A-37 Title: Perfect score:

1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 908470 seqs, 133250620 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_101002:* Database :

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:* /SIDS2/gcgdata/geneseg/genesegp-embl/AA1992.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1993.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseg/genesegp-embl/AA1997 DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA1998 DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*

SUMMARIES

		Description	H6FXTN23 fusion or	. Human tetranectin	H6FXTN123 fusion p	Human tetranectin.	Human EST encoded	CIIH6FXTN123 fusio	Sequence of chain	. Tetranectin polvoe	H6FXtripa fusion p	Tetranectin polype	
		ID	AAW94264	AAW94256	AAW94262	AAR60521	AAM24034	AAW94261	AAP60098	AAW94254	AAW94270	AAW94255	
		DB	20	20	20	15	22	20	7	20	20	20	
		Match Length DB	180	181	197	202	202	228	182	52	73	49	
r	Query	Match	85.4	85.4	85.4	85.4	85.4	85.4	82.5	79.5	79.5	74.9	
		Score	146	146	146	146	146	146	141	136	136	128	
	Result	NO.	1	7	m	4		9	7	80	6	10	

Etzerodt M, Graversen NJH, Holtet TL, Kastrup JS; Larsen IK, Nielsen BB, Thogersen HC;

(ETZE/) ETZERODT M. (GRAV/) GRAVERSEN N J H. (HOLT/) HOLTET T L. (KAST/) KASTRUP J S.

98WO-DK00245. 97DK-0000685

11-JUN-1998;

11-JUN-1997;

C 10 L E L C	മാ മ~തെ	00 0010	e #500 e #530 e #488 peptid gene p human i grow ' a Co pRO539 human alpha	
AAW94 AAW94 AAW94 AAW94 AAW94	AAB2852 AAU8264 AAY6675 AAU2916 AAB6527 AAE2046	ABP2817 ABP2593 ABB7114 ABB7035 ABB3240 ABB23178 AAM5849		
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ALIGNMENTS

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Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structura; toxin; enzyme; cytoKine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; H6FXTN23.
                  AAW94264 standard; protein; 180 AA
                                                                          H6FXTN23 fusion protein sequence.
                                                       26-APR-1999 (first entry)
                                                                                                                                                       Homo sapiens
                                                                                                                                                                          WO9856906-A1
                                                                                                                                                                                              17-DEC-1998.
                                                                                                                                              Synthetic
                                     AAW94264;
RESULT 1
AAW94264
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97DK-0000685

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11-JUN-1997;
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                                                                                                                                           The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein (Emily: The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimeric polypeptide construct comparise at least one tetranectin trimeric polypeptide construct comparise at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous moiety, the TTSE being capable of forming a stable complex with 2 other TTSEs, with the proviso that the heterologous moiety is different from any of the fusion proteins CIHGEXTN123, HGEXTN123, HGEXTN12 HGEXTN23 (AAMW94261) The TTSE can be used for the construction of conjugates with heterologous moleties such as a ligand binding structure, a toxin, a detectable label, an in situ activatable substance, an enzyme, a radioactive moiety, a cytchine, an on-proteinaceous polymer, or a proty facilitating conjugation of the paperic or a photo cross-linking agent, or a group facilitating conjugation of the operies for generating chimmer; artificial antibodies having constructs can be used for targeted gene therapy involving selective constructs can be used for transfection or infection of the specific population of cells. They can also be used for delivering a substance to a cell or tissue or for delivering an imaging or toxin-conjugated cat as a vehicle for a wide variety of conjugates. The present sequence cat as a vehicle for a wide variety of conjugates. The presents a HGEXTN23 fusion protein sequence. The specification claims the heterologous moiety to which the TTSEs of the invention are linked to is specifically different from the present fusion protein
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                                             New monomer polypeptide constructs for diagnosis and therapy - comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.4%; Score 146; DB 20; 180.6%; Pred. No. 2.9e-11; ive 6; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human tetranectin amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW94256 standard; protein; 181 AA.
                                                                                                                        Disclosure; Fig 8; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-DK00245
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              WPI; 1999-080897/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 AA;
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                                                                                          activity
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structure, a toxin, a detectable label, an in situ activatable substance, an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer, a photo cross-linking agent, or a group facilitating conjugation of the monomer polypeptide construct to a target. They can be used as vehicles for assembling antibody fragments into oligomeric or multivalent entities for generating chimeric artificial antibodies having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  population of cells. They can also be used for delivering a substance to a cell or tissue or for delivering an imaging or toxin-conjugated antibody to a tumour. They can also be used for prevention or treating a disease or for diagnosis. The TrSE provides a stable structure which can act as a vehicle for a wide variety of conjugates. The present sequence represents a human tetranectin sequence from which the TTSE can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytoKine; artificial antibody; pharmacoKinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; H6FXTN123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      element (TTSE) which is covalently linked to at least one heterologous molety, the TTSE being capable of forming a stable complex with 2 other TTSEs, with the proviso that the heterologous molety is different from any of the fusion proteins CIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN12 (AAW94261 to AAW94264). The TTSE can be used for the construction of conjugates with heterologous moleties such as a ligand binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preselected pharmacokinetic and/or pharmadynamic properties. The constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                      New monomer polypeptide constructs for diagnosis and therapy comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                            Kastrup JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.4%; Score 146; DB 20;
80.6%; Pred. No. 2.9e-11;
11ve 6; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
                                                                                                                                                                 NJH, Holtet TL,
                                                                                                                                                                                                        Thogersen HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 60; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW94262 standard; protein; 197 AA.
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ETZERODT M.
GRAVERSEN N J H.
HOLTET T L.
                                                                                                                                                                                                        Nielsen BB,
                                                                                                                                                                        Graversen
                                                                                                                                                                                                                                                                    WPI; 1999-080897/07.
                                                                                                  (KAST/) KASTRUP J S.
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                                                                                                                                                                     Etzerodt M,
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                                                                                                                                                                                                        Larsen IK,
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(ETZE/)
(GRAV/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                activity
                                                                  HOLT
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Human tetranectin
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                                                                                                                                                                                                                                                                                                                                 The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous moiety, the TTSE being capable of forming a stable complex with 2 other TTSEs, with the provise that the heterologous moiety is different from any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN2 (AAM94261 to AAM94264). The TTSE can be used for the construction of conjugates with heterologous moiety such as a ligand binding structure, a toxin, a detectable label, an in situ activatable substance, an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer, a photo cross-linking agent, or a group facilitating conjugation of the monomer polypeptide construct to a target. They can be used as vehicles for assembling antibody fragments into oligomeric or multivalent constructs can be used for transfection or milective constructs can be used for transfection or infection of the specific population of calls. They can also be used for delivering a substance to a call or tissue or for delivering an imaging or toxin-conjugated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody to a tumour. They can also be used for prevention or treating a disease or for diagnosis. The TTSE provides a stable structure which can act as a vehicle for a wide variety of conjugates. The present sequence represents a H6FXTN123 fusion protein sequence. The specification claims that the heterologous moiety to which the TTSEs of the invention are linked to is specifically different from the present fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                             New monomer polypeptide constructs for diagnosis and therapy comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
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                                                                                                                                                                                 Kastrup JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 146; DB 20;
Pred. No. 3.2e-11;
6; Mismatches 1;
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                                                                                                                                                                              JH, Holtet TL,
Thogersen HC;
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                                                                                                                                                                                                                                                                                                              Disclosure; Fig 6; 110pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.4%;
80.6%;
                                                               98WO-DK00245.
                                                                                      97DK-0000685
                                                                                                                                                                                Graversen NJH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                (ETZE/) ETZERODT M.
(GRAV/) GRAVERSEN N J H.
(HOLT/) HOLTET T L.
                                                                                                                                                                                             Larsen IK, Nielsen BB,
                                                                                                                                                       (KAST/) KASTRUP J S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 AA;
            W09856906-A1
                                                                                      11-JUN-1997;
                                                              11-JUN-1998;
                                    17-DEC-1998.
                                                                                                                                                                                Stzerodt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29;
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cDNA encoding human tetranectin (full sequence given in AAR6051) was PCR amplified cDNA was linked to a sequence encoding the Factor-Xa cleavage site (given in AAR60503), subcloned in vector pT7H6 so that it was linked to a hexahistidine-encoding sequence and expressed in E. coli BL1. The fusion protein was purified on an Ni2+-activated NTA-agarose column. A cyclic procedure was used to obtain correctly folded recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.4%; Score 146; DB 15; Length 202; 80.6%; Pred. No. 3.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Refolding of polypeptide molecules - using a cyclic process
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       denaturing and renaturing conditions to produce a
     tetranectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
Serine protease; Factor-Xa; recognition site; tet fusion protein cleavage; protein folding; primer; polymerase chain reaction; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human EST encoded protein SEQ ID NO: 1559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 151-52; 202pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thogersen HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM24034 standard; Protein; 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JAN-2001; 2001WO-US02687.
                                                                                                                                                                                                                                                                                                                                   93DK-0000130
                                                                                                                                                                                                                                                                                                                                                       93DK-0000139
93WO-GB02492
                                                                                                                                                                                                                                                                             94WO-DK00054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Etzerodt M, Holtet TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              correctly folded prod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-279681/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (DENZ-) DENZYME APS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200154477-A2.
                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                             14-FEB-1994;
                                                                                                                                                                                                                                                                                                                                04-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                05-FEB-1993;
03-DEC-1993;
                                                                                                                                                                                                                      L8-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2001
                                                                                                                                                                WO9418227-A.
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30-DEC-1986
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AAP60098
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                                                                                                                                                                     The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, foremsics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; CIIH6FXTN123.
                                                                                                                           Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                                                                                                                                                                               Gaps
                                                                           Asundi V;
                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                             Length 202;
                                                                                                                                                                                                                                                                                             Indels
                                                                          Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kastrup JS;
                                                                                                                                                                                                                                                                          Score 146; DB 22;
Pred. No. 3.3e-11;
6; Mismatches 1;
                                                                       Zhou P, Qian XB, Wang Z,
A, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                          1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                      Graversen NJH, Holtet TL,
Nielsen BB, Thogersen HC;
                                                                                                                                                      Claim 20; Page 1069; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             CIIH6FXTN123 fusion protein sequence.
                                                                                                                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                                                                                                                                                                                                                                          AAW94261 standard; protein; 228
                                                                                                                                                                                                                                                                          85.4%;
80.6%;
      25-JAN-2000; 2000US-0491404.
17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97DK-0000685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-DK00245
                                                                                                                                                                                                                                                                                                                                                                                                            26-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                          29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GRAV/) GRAVERSEN N J H. (HOLT/) HOLTET T L. (KAST/) KASTRUP J S.
                                                                                 Drmanac RA,
                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                               WPI; 2001-476164/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-080897/07
                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETZE/) ETZERODT M.
                                                                                                                                                                                                                                                        202 AA;
                                                                       Liu C,
                                                                                                           N-PSDB; AAH98693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9856906-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Etzerodt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Larsen IK,
                                                                                                                                                                                                                                                        Seguence
                                                                      Fang YT,
                                                                                                                                                                                                                                                                                                                                                                                           AAW94261;
                                                                                                                                                                                                                                                                         Query Match
                                                                                Cao Y,
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                 AAW9426.
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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein camily. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous construct comprise at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous conject, the TTSE bank the proviso that the heterologous moiety is different from TTSEs, with the proviso that the heterologous moiety is different from any of the fusion proteins CIH6FXTN123, H6FXTN12, H6FXTN13, H7FTSE provides a stable structure which can tail of the present sequence represents a CIH6FXTN13 fusion protein sequence. The present fusion protein sequence. Claims that the heterologous moiety to which the TTSEs of the Invention sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
New monomer polypeptide constructs for diagnosis and therapy comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasminogen activation; clot lysis; fibrinolysis; tissue growth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85.4%; Score 146; DB 20;
80.6%; Pred. No. 3.8e-11;
live 6; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue repair; haemostasis; neoplasia therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence of chain of Tetranectin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                 Disclosure; Fig 6; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP60098 standard; protein; 182 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.6 Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50..60
77.176
152..168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond 5
Disulfide-bond 7
Disulfide-bond 1
Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP206400-A.
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linked to at least one heterologous moiety for providing functional
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                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW94270;
            activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW94270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trimeric polypeptide; tetranectin trimerising structural element; TTSE; flusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin.
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                            formula shown in AAP60098. Tetranectin stimulates and controls the plasminogen activation resulting in a higher rate of clot lysis or fibrinolysis, esp. in the presence of blood platelets and in the presence of a complex fibrin clot from blood. It stimulates and controls the plasminogen activation in the absence of fibrin but in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New monomer polypeptide constructs for diagnosis and therapy comprise a tetranectin trimerising structural element covalently
                                                                                                                                                                    Tetranectin is comprised of four polypeptide chains having the
                                                                                                                                                                                                                                                                                          ;
0
                                                                                                        New Tetranectin protein - purified from human blood plasma by e.g. affinity chromatography on a column with coupled kringle of plasminogen
                                                                                                                                                                                                                                                                      Length 182;
                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kastrup JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Tetranectin polypeptide fragment (residues 1-52).
                                                                                                                                                                                                                                                                    Score 141; DB 7;
Pred. No. 1.3e-10;
6; Mismatches 2
                                                                                                                                                                                                                              the presence of a cofactor such as polylysine.
                                                                                                                                                                                                                                                                                                                      1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H, Holtet TL,
Thogersen HC;
                                                                                                                                                                                                                                                                                                                                                                               AAW94254 standard; Protein; 52 AA.
                                                                                                                                                 Claim 9; Page la; 12pp; English.
                                                                                                                                                                                                                                                                    82.5%;
77.8%;
         86EP-0201005.
                            85NL-0001682.
                                                                 Duhl Clemmensen I, Kluft C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-DK00245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97DK-0000685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NJH,
                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                (NEDE ) NEDERLAND ORG TNO.
                                                                                                                                                                                                                                                                               Best_Local Similarity 77.8
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ETZE/) ETZERODT M.
(GRAV/) GRAVERSEN N J H.
(HOLT/) HOLTET T L.
(KAST/) KASTRUP J S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Graversen Nielsen BB,
                                                                                     WPI; 1986-340760/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-080897/07
                                                                                                                                                                                                                                                  182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9856906-A1.
         10-JUN-1986;
                            11-JUN-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-DEC-1998
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                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 AAW94254;
                                                                                                                                                                                                                                                                     Query Match
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constitute Compilise a teast one telemettin timestainy structures.

Compilise a teast one telement a stable complex with 2 other TTSE being capable of forming a stable complex with 2 other TTSEs, with the proviso that the heterologous moiety is different from any of the fusion proteins CIIHGETAN123, HEFXTN123, HEFXTN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody to a tumour. They can also be used for prevention or treating a disease or for diagnosis. The TTSE provides a stable structure which can act as a vehicle for a wide variety of conjugates. The present sequence represents a human tetranectin polypeptide fragment. The encoding nucleic acid sequence was amplified by PCR from the plasmid clone pT7H6FXTN123. This is used in the construction of E. coll expression vectors for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin.
                                                                                                                      The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                           construct comprise at least one tetranectin trimerising structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   production of trimerised chimeric fusion proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 136; DB 20;
Pred. No. 1.4e-10;
6; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVSLK 52
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English.
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77.8%;
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Example 1; Page 59; 110pp;
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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein cample of Timeric polypeptides constructed as a monomer polypeptide constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologus on object, the TTSE being capable of forming a stable complex with 2 other TTSE, with the proviso that the heterologous molety is different from any of the fusion proteins CIHPERTNI23, HERYNI23, HERYNI23, HERYNI23, HERYNI23, CONJUGATES with heterologous moleties such as a ligand binding conjugates with heterologous moleties such as a ligand binding conjugates with heterologous moleties such as a ligand binding conjugates with heterologous moleties such as a ligand binding conjugated bencetable label, an in situ activatable substance, a photo cross-linking agent, or a group facilitating conjugation of the construct to a target. They can be used as vehicles of a sembling antibody fragments into oligomeric or multivalent constructs can be used for target or pharmacokinetic and/or pharmacokinetic and/or pharmacokinetic pharmacokine constructs can be used for targeted gene therapy involving selective constructs can be used for targeted gene therapy involving selective constructs can be used for targeted gene therapy involving selective constructs can be used for targeted gene therapy involving or toxin-conjugated antibody to a tumour. They can also be used for prevention or treating a callor to tissue or for delivering an imaging or toxin-conjugated cat as a vehicle for a wide variety of conjugates. The present sequence creates as a vehicle for a wide variety of conjugates. The present sequence or expresents a HERXTIDE function protein sequence encoded by the plasmid
                                                                                                                                                                                                                                                                                                                                                                               New monomer polypeptide constructs for diagnosis and therapy comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
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                                                                                                                                                      Graversen NJH, Holtet TL,
                                                                                                                                                                                                         Thogersen HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 4; 110pp; English.
                                                                                                                                                                                               Nielsen BB,
(HOLT/) HOLTET T L. (KAST/) KASTRUP J S.
                                                                                                                                                                                                                                                                                         WPI; 1999-080897/07
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                                                                                                                                                      Etzerodt M,
                                                                                                                                                                                                    Larsen IK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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     NAME OF COLOR COLO
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New monomer polypeptide constructs for diagnosis and therapy comprise a tetranectin trimerising structural element covalently linked to at least one heterologous molety for providing functional

Example 1; Page 59-60; 110pp; English.

Graversen NJH, Holtet TL, Kastrup JS;

98WO-DK00245. 97DK-0000685

11-JUN-1997; 11-JUN-1998;

GRAVERSEN N J H.

(KAST/) KASTRUP J S. HOLTET T L.

HOLT/ GRAV/)

Thogersen HC;

Nielsen BB,

Etzerodt M, Larsen IK, WPI; 1999-080897/07.

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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein construct comprise at least one tetranectin trimerising structural constructs. With the proviso that the heterologous moiety is different from any of the fusion proteins CIMERTAN13, HERTAN13, CC CONJUGATES WITH heterologous moieties such as a ligand binding structure, a detectable label, an in situ activatable substance. CC conjugates with heterologous moieties such as a ligand binding conjugation of the monomer polypeptide construct or a group facilitating conjugation of the operations and properties or a proup an ease as vehicles constructs can be used for target or multivalent constructs can be used for targeted gene therapy involving selective constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific coppulation of cells. They can also be used for prevention of the specific a collivery of the material for transfection or infection of the specific coppulation of cells. They can also be used for preventing a substance to a cell or tissue or for delivering an imaging or toxin-conjugated disease or for diagnosis. They can also be used for prevention of can confidence was a vehicle for a wide variety of conjugates. The present sequence confidence was amplified by PCR from the plasmid clone p77H6FXTN123. This is used in the construction of E. coll example in the construction of E. coll example in the construction of E. coll example in the construction of this 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTV 33
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Matches 26; Conservative
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AAW94263
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1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 36

28; Conservative

Matches

Local Similarity

Query Match

Tetranectin polypeptide fragment (residues 1-49).

Homo sapiens. WO9856906-A1 17-DEC-1998.

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26-APR-1999 (first entry)

AAW94255;

AAW94255 standard; Protein; 49 AA.

RESULT 10 AAW94255

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Length 73;

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Gaps

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AAW94271 standard; protein; 69 AA.

AAW94271

26-APR-1999 (first entry)

AAW94271;

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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous moiety, the TTSE being capable of forming a stable complex with 2 other TTSEs, with the provise that the heterologous moiety is different from any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN12 (AAM94261 to AAM94264). The TTSE can be used for the construction of conjugates with heterologous moiety as ligand binding structure, a toxin, a detectable label, an in situ activatable substance, an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer, a photo cross-linking agent, or a group facilitating conjugation of the monomer polypeptide construct to a target. They can be used as vehicles for assembling antibody fragments into oligomeric or multivalent preselected pharmacokinetic and/or pharmadynamic properties. The constructs can be used for transfection or infection of the specific population of cells. They can also be used for delivering a substance to a cell or tissue or for delivering an imaging or toxin-conjugated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New monomer polypeptide constructs for diagnosis and therapy comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; H6FXTN12.
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GRAVERSEN N J H.
HOLTET T L.
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                                                                                                                                                                                                               Homo sapiens.
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(GRAV/)
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                       74.9%; Score 128; DB 20; Length 65; 78.8%; Pred. No. 2e-09;
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65 AA;
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1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTV 33

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Query Match Best Local Matches 2

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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimeris polypeptide construct comprise at least one tetranectin trimeris polypeptide construct comprise at least one tetranectin trimeris polypeptide construct comprise at least one heterologous moiety, the TTSE being capable of forming a stable complex with 2 other TTSEs, with the proviso that the heterologous moiety is different from any of the fusion proteins CliHGTYN123, HGFXTN123, HGFXTN12, HGFXTN123 (AAW94261 to AAM94264). The TTSE can be used for the construction of conjugates with heterologous moieties such as a ligand binding structure, a toxin, a detectable label, an in situ activatable substance, an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer, a photo cross-linking agent, or a group facilitating conjugation of the monomer polypeptide construct to a target. They can be used as vehicles for assembling antibody fragments into oligomeric or multivalent entities for generating chimmeric artificial antibodies having the material for transfection or infection of the specific constructs can be used for transfection or infection of the specific
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                                                                                                                         Trimeric polypeptide; tetranectin trimerising structural element; TTSE; flusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin.
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                                                                                 H6FXtripb fusion protein sequence.
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(GRAV/) GRAVERSEN N
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                                                                                                                                                                                                                                   Synthetic
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Length 69; Score 124; DB 20; Pred. No. 7.2e-09; 72.5%; 78.1%; Query Match Best Local Similarity ; 0

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     Gaps
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Nielsen BB, Thogersen HC;
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 6; Mismatches
                                    32
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                                                  1 LVSSKMFEELKNRMDVLAQEVALLKEKQALQT
                                                                                                                                                                                                                                                           H6FXtripB-UB fusion protein sequence.
                                                                                                                                                      AAW94266 standard; protein; 145 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ETZE/) ETZERODT M.
(GRAV/) GRAVERSEN N J H.
(HOLT/) HOLTET T L.
(KAST/) KASTRUP J S.
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25;
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Matches
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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous moiety, the TTSE being capable of forming a stable complex with 2 other TTSEs, with the provise that the heterologous moiety is different from any of the fusion proteins CIHGEXTN123, HGEXTN123, HGEXTN12, HGEXTN3 CONJUGATES with heterologous moieties such as a ligand binding structure, a toxin, a detectable label, an in situ activatable substance, an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer, a photo cross-linking agent, or a group facilitating conjugation of the monomer polypeptide construct to a target. They can be used as vehicles for assembling antibody fragments into oligomeric or multivalent
act as a vehicle for a wide variety of conjugates. The present sequence represents a H6FXtripB-UB (ubiquitin) fusion protein sequence encoded by the plasmid pH6FXtripB-UB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; CEA6.
                                                                                                                                                         Gaps
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                                                                                                                 Length 145;
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                                                                                                                   20;
                                                                                                                 Score 124; DB 20;
Pred. No. 1.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                              H6FXscFv(CEA6)tripB fusion protein sequence.
                                                                                                                                  Pred. No. 1.7e
6; Mismatches
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                                                                                                           Query Match 72.5°
Best Local Similarity 78.1°
Matches 25; Conservative
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(HOLT/) HOLTET T L.
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                                                                            145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                               preselected pharmacokinetic and/or pharmadynamic properties. The constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific population of cells. They can also be used for delivering a substance to a cell or tissue or for delivering an imaging or toxin-conjugated antibody to a tumour. They can also be used for prevention or treating a disease or for diagnosis. The TTSE provides a stable structure which can act as a vehicle for a wide variety of conjugates. The present sequence represents a HGFXSCFV(CEA6)tripB fusion protein sequence encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to the design of trimeric polypeptides using polypeptide structural alements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural element (TYES) which is covalently linked to at least one heterologous moiety, the TYSE being capable of forming a stable complex with 2 other TYSEs, with the proviso that the heterologous moiety is different from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; CEA6.
                                                                                                                                                                                                                                                                                                      Gaps
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generating chimeric artificial antibodies having
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                                                                                                                                                                                                                                                               72.5%; Score 124; DB 20; Length 330; 78.1%; Pred. No. 4.2e-08; 1ive 6; Mismatches 1; Indels
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Nielsen BB, Thogersen HC;
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                                                                                                                                                                                             plasmid pH6FXscFv(CEA6)tripB
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(HOLT/) HOLTET T L.
(KAST/) KASTRUP J S.
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nes 25; Conserv
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AMM94261 to AAM94264). The TTSE can be used for the construction of conjugates with heterologous moieties such as a ligand binding structure, a toxin, a detectable label, an in situ activatable substance, an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer, a photo cross-linking agent, or a group facilitating conjugation of the monomer polypeptide construct to a traget. They can be used as vehicles for assembling antibody fragments into oligoment or multivalent entitles for generating chimeric artificial antibodies having preselected pharmacokinetic and/or pharmadynamic properties. The constructs can be used for transfection or infection of the specific population of cells. They can also be used for delivering a substance to a cell or tissue or for delivering an imaging or toxin-conjugated antibody to a tumour. They can also be used for prevention or treating a mitbody to a tumour. They can also be used for prevention or treating a disease or for diagnosis. The TTSE provides a stable structure which can a tas a vehicle for a wide variety of conjugates. The present sequence encoded by the
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of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN23
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78.1%;
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17 116 3 116 5 5

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Q9NG11 Q96754 Q992X9 Q00210

448 232 278 509 635 654 857

Q81590 methanosarc 006302 mycobacteri Q41556 triticum ae 053030 enterococcu

54.5 54.5 54.5 54.5 53.5 53.5 53.5

O22909 arabidopsis

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April 15, 2003, 11:44:50 ; Search time 22.5 Seconds (without alignments) 329.675 Million cell updates/sec
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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172
1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK
                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                           671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                    summaries
                                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

08x14 pyrobaculum 015154 homo sapien 090304 breda virus 095849 homo sapien 09x2k9 drosophila 09x164 arabidopsis 000867 plasmodium 08x1n6 clostridium Q9ddd4 gallus gall Q9epw4 mus musculu Q28008 bos taurus O14689 homo sapien Q8z110 salmonella Q8z212 salmonella Q8r8c6 thermoanaer Q9lm53 arabidopsis Description O14689 Q82VH4 O9W2K9 Q9LFE4 08ZL10 08Z2L2 08Z8C6 08R8C6 09LM53 **OBXLN6** 090304 028008 000867 Length 201 196 197 761 761 794 1978 1583 Query Match 1 123 84 79 60 60 60 59 58 58 57.5 57.5 57 57 57 56 56 Score Result Š.

RESULT 09DDD4	JLT 1 DD4					
Ω	Q9DDD4	PRELIMINARY;	PRT;	201 AA.		
AC	Q9DDD4;					
DT	01-MAR-2001	(TrEMBLrel. 16,	Created)			
DŢ	01-MAR-2001		Last seq	16, Last sequence update)	ate)	
DŢ	01-DEC-2001	(TrEMBLrel. 19,	Last	annotation update)	odate)	
DE	Tetranectin.					
OS	Gallus gallu	Gallus gallus (Chicken).				
8	Eukaryota; M	fetazoa; Chordata	; Crania	ta; Vertel	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
ဗ	Archosauria;	Aves; Neognatha	e; Galli	formes; P	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	
8	Gallus.					
ŏ	NCBI_TaxID=9031;	1031;				
RN	Ξ					
RP	SEQUENCE FROM N.A.	M N.A.				
RA	Wewer U.M.;					
RŢ	"tetranectin	"tetranectin in chicken.";		•		
RL	Submitted (N	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases	EMBL/Gen	Bank/DDBJ	databases.	
DR	EMBL; AJ2771	EMBL; AJ277116; CAC20217.1;				
DR	HSSP; P05452; 1TN3.	2; 1TN3.				
DR	InterPro; IF	InterPro; IPR001304; Lectin_C.				
DR	Pfam; PF0005	Pfam; PF00059; lectin_c; 1.				
DR	SMART; SMOOC	SMART; SM00034; CLECT; 1.				
: DR	PROSITE; PSC	0615; C_TYPE_LEC	TIN_1; 1			
DR	PROSITE; PS5	PROSITE; PS50041; C_TYPE_LECTIN_2;	TIN_2; 1			
SO	SEQUENCE 2	201 AA; 22172 MW	1; 7C7F2	22172 MW; 7C7F235D24426AE8 CRC64;	38 CRC64;	
OBE	Query Match Best Local Similarity Matches 24: Conserv	71.5%; 68.6%; ative		Score 123; DB 13; Pred. No. 1e-07; 7: Mismatches 4:	3; Length 201; 4: Indels 0: Gaps	ë.
į	TOWNS C	TANED A THE CONTRACT				
Š	Z VNTKMFE	Z VNIKMFEELKSKLUILAQEVALLARQQALQIVCLA	A ECCALCT	VCLK 30		
qa	38 VSLKMIE	VSLKMIEDLKAMIDNISQEVALLKEKQALQTVCLK	KEKQALQT	VCLK 72		
RESULT	JLT 2					
OYEPW4	W4 Q9EPW4	PRELIMINARY;	PRT;	196 AA.		
ŀ						

761 AA.

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Abe A., Emi N., Tanimoto M., Terasaki H., Marunouchi T., Saito H.; "Fusion of the platelet derived growth factor receptor beta to a no gene CEVIA in acute myelogenous leukemia after clonal evolution."; Blood 90:4277(199).
                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomí;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER 1 1 SEQUENCE 761 AA; 87160 MW; 75DD86243E9F0CF5 CRC64;
                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 34.9%; Score 60; DB Best Local Similarity 44.1%; Pred. No. 30; Matches 15; Conservative 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98043615; PubMed-9373237;
                                                                                 PRELIMINARY;
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"Mouse homolog of human CLECSF1, a cartilage derived C-type lectin.";
Submitted (OGT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: 87317204; A6448620.1; -.
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidea; Bovinee; Bos.
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Neame P.J., Boynton R.E.;
Neame P.J., Boynton R.E.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: U22298; AAC18614.1; -.
EMBL: PSO00519; Lectin_C;
Pfam; PF00059; lectin_C;
Pfam; PF00059; Lectin_C;
PROSTIE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 45.9%; Score 79; DB 6; Length 197; Best Local Similarity 57.1%; Pred. No. 0.032; Matches 16; Conservative 7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 196 AA; 22191 MW; 9AE4C809D119E852 CRC64;
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CHAIN 25 197 C-TYPE LECTIN HOMOLOG.
SEQUENCE 197 AA; 22215 MW; AAAC4280F41ACOF4 CRC64;
                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
C-type lectin superfamily 1.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
C-type lectin homolog precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 EELKSRLDTLAQEVALLKEQQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 DDLKSQVEKLWREVNALKEMQALQTVCLR 70
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                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                      STRAIN-ES129/SV;
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Lectin; Signal.
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Matches
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DB 4; Length 761; 30;

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                                                                                                                                                                                                                                                                                                                                                                     Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I., Miller J.H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete proteome.
SEQUENCE 794 AA; 91123 MW; 530347055A96034C CRC64;
                                                                                                                                                                                                  Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   aerophilum.";
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL, AE009967; AAL64082.1; -
INTERPTO; IPR002106; AALRNA_ligaseII.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR003739; Euk_Pkinase.
InterPro; IPR003395; SMC_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.9%; Score 60; DB 17;
54.5%; Pred. No. 31;
ive 6; Mismatches 4
794 AA
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STRAIN-IM2 / ATCC 51768 / DSM 7523;
PubMed=11792869;
  PRT;
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                                                                                                                                                                                                                            Thermoproteaceae; Pyrobaculum
                                                                                                                   Hypothetical protein PAE2280. PAE2280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 54.5
Matches 12; Conservative
PRELIMINARY;
                                                                                                                                                                          Pyrobaculum aerophilum.
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Golgi-associated microtubule-binding protein
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nes 15; Conserv
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                                                                        SEQUENCE FROM N.A.
                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                 CG9415 protein.
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          GMAP-210
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                                                                                                                                                                                             Matches
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Duckmanton L.M., Tellier R., Liu P., Petric M.;
"Bovine torrovirus: sequencing of the structural genes and expression of the nucleocapsid protein of Breda virus.";
Virus Res. 58:88-96(1998).
EMBL; AF076621; AAD03840.]; -.
SEQUENCE 1583 AA; 177785 MW; 0529C1293B38849C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                               MEDLINE=97404344; PubMed=9256431;
Chang K.H., Chen Y., Chen T.T., Chou W.H., Chen P.L., Ma Y.T.,
Yang-Feng T.L., Leng L., Tsai M.J., O'Malley B.W., Lee W.H.;
"A thyroid hormone receptor coactivator negatively regulated by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Torovirus.
                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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48.1%; Pred. No. 84;
tive 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                 Score 60; DB 4; Length 1978;
Pred. No. 79;
5; Mismatches 12; Indels
                                                                                                                                                                                                                          retinoblastoma protein.";
Proc. Natl. Acad. Sci. U.S.A. 94:9040-9045(1997).
EMBL; AF007217; AAD09135.1;
SEQUENCE 1978 AA; 227514 MW; AACB4EB45C75FD7E CRC64;
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Last sequence update)
Last annotation update)
                                                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                        1583 AA.
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095949;
01-MAY-1999 (TrEMBLRel. 10, C:
01-MAY-1999 (TrEMBLRel. 10, L:
01-DEC-2001 (TrEMBLRel. 19, L:
                                                                                                                                                                                                                                                                                Query Match 34.9%;
Best Local Similarity 44.1%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 48.1
Matches 13; Conservative
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                                          PRELIMINARY;
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                                                                                                                                                   NCBI_TaxID=9606;
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                  RESULT 6
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090304
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095949
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RAM Adams M.D., Celliker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celliker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Scherer S.E., Holf R.A., Hoskins R.A., Galle R.F.,
RA Gocage R.A. Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandeall M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Mortman J.R., Yandeall M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Ragers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Apdayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Dockova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Dockova D., Botcher A., Deng Z., Mays A.D., Dew I., Daietz S.M.,
RA Dockon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dockon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dockon K., Doup L.E., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Eosler C., Gabriellan A.E., Garry N.S., Reriters S., Pfelsischmann W.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Lasko P., Lei Y., Levitsky T.A., Howland T.J., Mei M.-H., Ibegwam C.,
RA Lasko P., Lei Y., Levitsky T.A., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky T.A., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky T.A., Li Z., Liang Y., Lin X.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzriy D., Puzi V., Pacese M.G.,
RA Raincett K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Stemfigton K., Saunders R.D.C., Scheeler F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Strong R., Strong R., Spier E., Shen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                               Infante C., Ramos-Morales F., Fedrianl F., Bornens M., Rios R.M.; "GMAP-210, a C1S-Golgi network-associated protein, is a minus end microtubule-binding protein.";
J. Cell Biol. 145:83-9959(1999).

EMBL; Y12490; CAA730951;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1979 AA; 227639 MW; 83E46777D34D360D CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 59; DB 4; Ler
Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                               MEDLINE=99207053; PubMed=10189370;
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ilarity 44.1%;
Conservative
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Guntaka R.V., Kandala J.C., Reddy V.D.;
"Cloning and characterization of a highly conserved HMG-like protein
(PFIG) gene from plasmodium falciparum.";
Biochem. Biophys. Res. Commun. 182:412-419(1992).
                                                                                                                                                                                                                                                                                                                                                              SERZIN-HB3:
Nambiar A., Kandala J.C., Dolan S.A., Jensen J.J., Guntaka R.V.;
Naccular cloning and characterization of a cDNA for the highly
conserved HMG-like protein (Pf16) gene of Plasmodium falciparum.";
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: U97128; AAB58115.1;
Hypothetical protein.
SEQUENCE 279 AA; 32106 MW; B44E9E202191C432 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridium.
                                                                                      Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     309 AA; 36468 MW; 62C34557D95C8A1C CRC64;
            01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Hypothetical 32.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

EMBL: AP003189; BAB80711.1; -.

InterPro; IPR002523; CorA.

Ocmplete proteome.

SEQUENCE 309 AA; 36468 MW; 62C34557D95C8AIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 57.5;
Pred. No. 22;
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48.0%; Pred. No. 24;
ive 10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 46.44
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium perfringens
                                  Hypothetical 32.1 kDa Plasmodium falciparum.
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STRAIN=13 / TYPE A;
PubMed=11792842;
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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01-MAR-2002 (
01-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query For Best Local Similar
                                                                                                                                                                                    STRAIN-HB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OBXLN6;
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ID Q8
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Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodager T., Worley K.C., Wu D., Yang S., Yao Q.A., Zeng J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).

-I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

-I- SIMILARITY: BELONGS TO THE BZIP FAMILY.

HSSP: P05412: IPOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 17, Last annotation update)
Hypothetical 96.2 kDa protein.
F5E19.70.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids 11; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X., Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Length 853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.7%; Score 58; DB 5; Length 488; 48.1%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL391147; CAC01837.1; -.
InterPro; IPR002017; Spectrin.
SWART; SM00150; SPEC; 1.
Hypothetical protein.
SEQUENCE 853 AA; 96207 MW; EB7563A667F11AAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      C05AD488DE404A59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 04, Created)
(TrEMBLrel. 04, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 NEKEVEKLKSELETVKEEKNRALKKEQDATSRV 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 ELKSRLDTLAQEVALLKEQQALQTVCL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                               PROSITE, PS00036, BZIP_BASIC, 1.
DNA-binding, Nuclear protein.
SEQUENCE 488 AA; 52359 MW; C
                                                                                                                                                                                                                                                                                                                  InterPro; IPR004827; TF_bZIP.
Pfam; PF00170; bZIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.7%;
48.5%;
                                                                                                                                                                                                                                                                                    FlyBase; FBgn0021872; xbp1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 48.1 tes 13, Conservative
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                         SMART; SM00338; BRLZ;
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01-JUL-1997 (
01-JUL-1997 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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000867
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DB 5; Length 279; Indels ij

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DB 16; Length 309;

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Pfam; PF03466; LysR_substrate; 1.
                                  PRINTS; PR00039; HTHLYSR
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Q8R8C6
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                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-LTZ / SGSC1412 / ATCC 700720;
MEDLINE-2134948; PubMed-11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                        01-NAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Transcriptional activator (LysR family).
DSDC OR SFM3800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
D-serine deaminase activator.
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33.1%; Score 57; DB 16;
Best Local Similarity 44.8%; Pred. No. 28;
Matches 13; Conservative 6; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00126; HTH_1; 1.
Pfam; PF03466; LysR_substrate; 1.
PRINTS; PR00039; HTHLYSR.
PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 AA.
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MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 413:852-856(2001).
EMBL; AE008877; AAL22660.1; -.
InterPro; IPR000847; HTH_LysR.
InterPro; IPR005119; LysR_subst.
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                                                                                                                                                                                              Salmonella typhimurium
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SEQUENCE 307 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                NCBI_TaxID=602;
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Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                       Gaps
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                                                 DB 16; Length 307; 28;
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Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Indels
                                                                                    10; Indels
PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.
Complete protecome.
SEQUENCE 307 AA; 35057 MW; 093B234FBF2F828C CRC64;
                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein TTE2080.
                                                                                                                                                                                                                   185 AA
                                                                                     6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Mismatches
                                                       Score 57;
Pred. No.
                                                                                                                                 5 KMFEELKSRLDTLAQEVALLKEQQALQTV 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: April 15, 2003, 11:50:09 Job time: 25.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 NTKMFEELKSRLDTLAQEVALLKEQQ 28
                                                                                                                                                                                                                                                                                                                        Thermoanaerobacter tengcongensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.6%;
                                                       33.1%;
                                                   Query Match
Best Local Similarity 44.89
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 42.33
Matches 11; Conservative
                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 15, 2003, 11:44:09; Search time 6.5 Seconds (without alignments) 229.715 Million cell updates/sec Run on:

US-09-445-576A-36 172 1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	452	mus m	P26258 carcharhinu	075596 homo sapien	P46068 escherichia	Q9kqn4 bacillus ha	Q10006 caenorhabdi	Q58794 methanococc		. Q9pm63 campylobact	7	P46939 homo sapien	neur	P18848 homo sapien	ther	œ		P47056 saccharomyc						/ bacil	Q92974 homo sapien) homo	sacch	-	Q9zcr3 rickettsia	P03030 escherichia		00 fowlpox	P19527 rattus norv
SUMMARIES	,	QI	TETN_HUMAN	TETN_MOUSE	TETN_CARSP	CLF1_HUMAN	DSDC_ECOLI	SYS_BACHD	YRY2_CAEEL	YD99_METJA	RM13_YEAST	RF1_CAMJE	YE33_SYNY3	UTRO_HUMAN	DYHC_NEUCR	ATF4_HUMAN	RA50_THEVO	A1A3_CHICK	YKR9_YEAST	YJD7_YEAST	CYSE_SYNY3	TNF5_FELCA	MYOC_HUMAN	SYA_SYNY3	Y419_HUMAN	YHCW_BACSU	GEFH_HUMAN	KINN_HUMAN	DPOE_YEAST	RL29_RICCN	RL29_RICPR	LYSR_ECOLI	m	V110_FOWPV	NFL_RAT
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		Length	202	202	166	197	311	425	252	197	275	355	524	3433	4367	351	895	1010	619	224	249	260	504	877	991	220	893	1032	2222	71	71	311	425	451	541
đ	Query	Match	100.0	84.9	ω.			32.6		30.8							29.7	29.7	29.4	29.1	29.1	29.1	29.1	29.1	29.1	28.8	28.8	æ	ω.	8	ω.	ω.	ω.	28.5	œ
	(Score	172		84	75	57	S	55.5	S	52.5	52	52	52	51.5	51	51	51	50.5	20	20	20	50	20	ς,	ģ	6	6	•					49	4. V
	Result	S	1	7	m	4	S	9	7	&	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P08551 mus musculu P35616 xenopus lae	P02547 sus scrofa P02548 bos taurus	Q26789 trypanosoma P11311 mycoplasma	Q60675 mus musculu O29230 archaeoglob	Q9ulvO homo sapien P21249 onchocerca	P48232 saccharomyc	P96769 actinobacil
NFL_MOUSE NFL_XENLA	NFL_PIG NFL_BOVIN	PFR2_TRYBB ADP1_MYCPN	LMA2_MOUSE RA50_ARCFU	MY5B_HUMAN ANT1_ONCVO	YNI6_YEAST	YHBJ_ACTAC
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542	548 554	595 1627	3106 886	1260 2022	102	110
28.5	28.5	28.5 28.5	28.5 28.2	28.2	27.9	27.9
4 4	0 4 0 0 6	4.4 0.0	49 48.5	48.5 48.5	48	48
34 35	37	38 30 8	4 0	4 4 3 2	44	45

ALIGNMENTS

RETTAN RETTAN RETTAN RETTAN RESTRICT TO COOO COOO COOO COOO COOO COOO COO	RESULT I TETN. HUNAN TO 105422. TO 10-NOV-1988 (Rel. 09, Created) DE 01-ARP-1993 (Rel. 109, Created) Tetranectin precursor (TN) (Plasminogen-Kringle 4 binding protein). THE OFFICE FROM N.A. REPUINE-920545; PubMed-134271; REPUINE-920545; PubMed-134271; REPUINE-920545; PubMed-131740; REPUINE-920545; PubMed-1511740; REPUINE-920545; PubMed-1511740; REPUINE-92066; PubMed-1511740; REPUINE-92066; PubMed-1511740; REPUINE-92066; PubMed-1511740; REPUINE-9207 Repuine Structure of tetranectin, a plasminogen binding protein.*; REPUINE-9208 Repuine Structure of tetranectin, a plasminogen kringle 4 binding Repuine-9208 Repuine Repuine-9200; Repuine-94200; Repuine-94200
R R R R R R R R R R R R R R R R R R R	PARTIAL SEQUENCE, MASS SPECTROMETRY, AND VARIANT GLY-106. TISSUE=Plasma; MEDLINE=20080486; PubMed=10614823; Jaquinod M., Holtet T.L., Etzerodt M., Clemmensen I., Thoegersen H.C., Roepstorif P.;
RT.	"Mass Spectrometric characterisation of post-translational modification and genetic variation in human tetranectin."; Biol. Chem. 380:1307-1314 (1999).

Biol. Chem. 380:1307-1314(1999). [7] R R -

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TETN_MOUSE
                                                                                   P43025;
                                                   TETN_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation. The European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE=97398360; PubMed=9256258;
Nielsen B.B., Kastrup J.S., Rasmussen H., Holtet T.L., Graversen J.H.,
Etzerodt M., Thoegersen H.C., Larsen I.K.;
Crystal structure of tetranectin, a trimeric plasminogen-binding
protein with an alpha helical coiled coil.";
FEBS Lett. 412:388-396(1997).
                                                                                                                                                          Kastrup J.S., Nielsen B.B., Rasmussen H., Holtet T.L., Graversen J.H., Etzerodt M., Thoegersen H.C., Larsen I.K.;
"Structure of the C-type lectin carbohydrate recognition domain of human tetranectin.";
Acta Crystallogr. D 54:757-766(1998).
-I- FUNCTION: Tetranectin binds to plasminogen and to isolated kringle 4. May be involved in the packaging of molecules destined for
                                                                                                                                                                                                                                                                                   -1- SUBUNIT: Homotrimer.
-1- SUBCELLULAR LOCATION: Secreted.
-1- MASS SPECTROMETRY: MW-20535.8; MW_ERR=2.4; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001304; Lectin_C.
Pfam: PF00059; lectin_c; 1.
SMART; SM0034; CLECT: 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
Lectin; Plasma; Signal; Polymorphism; Glycoprotein; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 202;
                                                                                                                                                                                                                                                                                                                                 RANGE-22-202.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2B0DCB5DF22E1AB8 CRC64;
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A -> S.
/FTIG=VAR_004189.
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                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 66-202.
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/FTId-VAR_004190
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/FTId=VAR_012318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, X70910; CAA50265.1; -. EMBL, X70911; CAA50265.1; JOINED. EMBL, X70912; CAA50265.1; JOINED. EMBL, X709124; AA411024.1; EMBL, X64559; CAA45860.1; EMBL, X6411.24.1; EMBL, X98121; CAA66803.1; -. PIR, S19865; S19865.
                                                                                                                                               MEDLINE-98437604; PubMed-9757090;
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Best Local Similarity 100.0
Matches 36; Conservative
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PDB; 1TN3; 06-MAY-98.
Genew; HGNC:11891; TNA.
MIM; 187520;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetranectin precursor (TN) (Plasminogen-kringle 4 binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BALB/C;
MEDLINE=96116955; PubMed=8563165;
Ibaraki K., Kozak C.A., Wewer U.M., Albrechtsen R., Young M.F.;
"Mouse tetranectin: CDNA sequence, tissue-specific expression, and
                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exocytosis (By similarity).
-- SUBDENT: Homotriner (By similarity).
-- SUBCELLULAR LOCATION.
-- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN LUNG AND SKELETAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-C57BL/6 x CBA; TISSUE-Lung;
MEDLINE-5737396; Pubmed-7835708;
Soerensen C.B., Berglund L., Petersen T.E.;
"Cloning of a cDNA encoding murine tetranectin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         r -> VI (IN REF. 2).
-> T (IN REF. 2).
                                                   01-NOV-1995 (Rel. 32, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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BY SIMILARITY.
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Plasma; Signal.
SIGNAL 1 21 BY SIMILA
  PRT;
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EMBL; U08555; AAA96811.1; -.
EMBL; X98122; CAA66804.1; -.
HSSP; P05422; ITWN.
MGD; MGI:104540; Tna.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mamm. Genome 6:693-696(1995).
STANDARD;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-type lectin superfamily member 1 precursor (Cartilage-derived C-type
                                                                                                                  Gaps
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Blasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Carcharhinidae; Carcharhinus.
NCBI_TaxID=7809;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0
                                                                             Length 202;
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 -> R (IN REF. 2).
-> Q (IN REF. 2).
639E7334D58EB04E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18432 MW; 53EF812DEA5C6119 CRC64;
                                                                                           80.6%; Pred. No. 3.1e-11;
Live 6; Mismatches 1;
                                                                           Score 146; DB 1;
                                                                                                                                                                                                                                                                                                                     01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tetranectin-like protein.
                                                                                                                                                                      1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
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Pfam; PF00059; lectin_c; 1.
PR0051F; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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                                     22257 MW;
                                                                           84.98;
                                                                                           Local Similarity 80.6
nes 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                   188 1
202 AA;
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166 AA;
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P26258;
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Matches
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96062227; PubMed=7592420;
Noerregaard-Madsen M., McFall E., Valentin-Hansen P.;
"Organization and transcriptional regulation of the Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-TYPE LECTIN SUPERFAMILY MEMBER 1. C-TYPE LECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 75; DB 1;
Pred. No. 0.019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSDC_ECOLI STANDARD; PRT; 311 AA. P46068; P77443; 01-NOV-1995 (Rel. 32, Created) 10-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) D-serine deaminase activator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                            EMBL; AF077345; AAD12542.1; -... EMBL; AF077344; AAD12542.1; -... EMBL; P05452; 1HTN. Genew; HGNC:2052; CLECSF1. InterPro; IPR001304; Lectin_C: Pfam; PF00059; lectin_C: 1... PROSITE; PS00615; C_TYPE_LECTIN_1; 1... PROSITE; PS00615; C_TYPE_LECTIN_1; 1... Lectin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 ELKSRLDTLAQEVALLKEQQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 177:6456-6461(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 PO
197 C-
192 C-
78 BY
191 BX
22232 MW;
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ilarity 57.1%;
Conservative
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74 1
68 95 1
167 1
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NCBI_TaxID=86665;
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Q10006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gardner A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YRY2_CAEEL
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                                                                                                                                                                                                                                                                                                                "Construction of a contiguous 874-kb sequence of the Escherichia coli - K12 genome corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features.";

DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D90866; BAA16223.1; ...
EMBL; D90866; BAA16224.1; ...
EMBL; N86379; ...
EMBL; A86379; ...
InterPro; IPR000847; HTH_LysR.
InterPro; IPR00199; LysR_subst.
Pfam; PF00126; HTH_1; 1...
Pfam; PF00126; LysR_substrate; 1...
PRINTS; PR00039; HTHLYSR.
PROSTE; PS00044; HTH_LYSR_FAMILY; 1...
Transcription regulation; DNA-binding; Activator; Complete proteome.
DNA_BIND 32 51 H-T-H WOTIF (POTENTIAL).
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                                                                                                                                                                             Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S., Tagami H., Takabhashi H., Takeda J., Takemoto K., Uehara K., Wada C., Yamagata S., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Seryl-than synthetase (EC 6.1.1.11) (Serine--tRNA ligase) (SerRS).
Bacillus halodurans.
Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: REGULATES THE EXPRESSION OF THE DSD OPERON FOR
D-SERINE DEAMINASE (DSDA).
-!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.1%; Score 57; DB 1; Length 311; 41.9%; Pred. No. 5; ive 7; Mismatches 11; Indels
                                        "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A -> R (IN REF. 1).; 0335B060CF5DB3BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            425 AA
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77 RVYWALKSSEDTLNOEIEDIKNOEESGTETE 107
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                                                                                                                                                          MEDLINE-97349980; PubMed-9205837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X91821; CAA62931.1; -. EMBL; AE000324; AAC75423.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35332 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-53 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 41.9
nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 AA;
                                                                                                           SEQUENCE FROM N.A.
Gregor J., Davis
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGULATORS
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Q9KGN4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=K12
                                                                                                                                       STRAIN-K12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                    "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000): - CATALYIC ACTIVITY: AP+ L-serine + tRNA(Ser) = AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                 + L-seryl-tRnA(Ser).
-- SUBUNIT: Homodiner (19 similarity).
-- SUBURIT: Homodiner (29 similarity).
-- SUBCELULAR LOCATION: Cycoplasmic.
-- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00981; TRNASYWTHSER.
TIGRFAMS; TIGR00414; serS; 1.
PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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                                                                                                Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masul
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 29.4 kDa protein T15H9.2 in chromosome II.
T15H9.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 AA; 48541 MW; DB4F2EDA0EEDE676 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.6%; Score 56; DB 1;
57.1%; Pred. No. 9.1;
iive 5; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002106; AAtRNA_ligaseII.
InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR002317; tRNA-synt_ser.
Pfam; PF00587; tRNA-synt_2b; I.
Pfam; PF005403; Seryl_tRNA_N; I.
SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE-20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 EELKSRLDTLAQEVALLKEQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 32.6
Best Local Similarity 57.1
Matches 12; Conservative
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CONFLICT
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RF1_CAMJE
ID RF1_C.
AC Q9PM6
DT 15-JU
DT 15-JU
DE Pepti
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSW 2661 / ATCC 43067;
MEDLINE-96337999; Pubmed-8688087;
Bult C.J., White O., Olson G.J., Eleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlawage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinston J.-F., Puhrmann J.E., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                     Gaps
                                                                                                                    1;
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                                                                                       ch 32.3%; Score 55.5; DB 1; Length 252; 1 Similarity 51.9%; Pred. No. 6.2; 14; Conservative 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.8%; Score 53; DB 1; Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 15 ATP (BY SIMILARITY).
197 AA; 22630 MW; A440F8259920F873 CRC64;
                                                                                                                                                                                                                                                                                                                                         Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                              252 AA; 29376 MW; 55AB2BA5F29414D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; ATP-binding; Complete proteome, NP_BIND 8 15 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Januaczania
Science 273:1058-1073(1996).
-!- SIMILARITY: BELONGS TO THE UPF0200 FAMILY.
                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                     197 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
or send an email to license@isb-sib.ch)
                                                                                                                                                        |:|||:|
EQLKSQLSRLDSSVAILKSQQMAVKSV 147
                                                                                                                                           8 EELKSRLDTLAQEVALLKEQQ-ALQTV 33
                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 VVNEKSFEDCLNQLDNILQEI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VVNTKMFEELKSRLDTLAQEV 21
                      EMBL; Z47356; CAA87415.1; -. WormPep; T15H9.2; CE01665.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U67580; AAB99408.1; -. TIGR; MJ1399; -.
                                                                                                                                                                                                                                                                                                  Hypothetical protein MJ1399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.68;
                                                                                                                                                                                                                                                                                                                             Methanococcus jannaschii.
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Best Local Similarity 47.6
Matches 10; Conservative
                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                    Best Local Similarity
Matches 14; Conserve
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-2190;
                                                                                                                                                                                                                                   YD99_METJA
Q58794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RM13_YEAST
Q02204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jannaschi1
                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RM13_YEAST
ID RM13_YE
AC Q02204;
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 SORBROS
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                                                                                                                                                                                                                                                                                                                 STRAIN-S288c;
MEDLINE=93070612; PubMed=1441752;
Duesterhoeft A., Philippsen P.;
"UnA sequencing and analysis of a 24.7 kb segment encompassing centromere CEN11 of Saccharomyces cerevisiae reveals nine previously unknown open reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria."; FEBS Lett. 204:51-56(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin
                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3,
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01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
60S ribosomal protein L13, mitochondrial precursor (YmL13).
MRPL13 OR YKROÜGC OR YK105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grohmann L., Kitakawa M., Isono K., Goldschmidt-Reisin S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MITOCHONDRION. 608 RIBOSOMAL PROTEIN L13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A -> S (IN REF. 2).
41F26BAA236E8B26 CRC64;
                                                                                                                                                                                                          Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ribosomal protein; Mitochondrion; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Peptide chain release factor 1 (RF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VVNTKMFEELKSRLDTLAQEVALLKE---QQALQT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.5%; Score 52.5; 37.1%; Pred. No. 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Mitochondrial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91285106; PubMed~2060626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 AA; 31526 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X65124; CAA46246.1; -. EMBL; X73673; CAA52022.1; -. EMBL; Z28231; CAA82076.1; -. PIR; S25816; S35816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGD; S0001714; MRPL13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [3]
SEQUENCE OF 87-120.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3est Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=07173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIBOSOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Graack H.-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RF1_CAMJE
Q9PM63;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                reveals hypervariable sequences.";
Nature 40:665-668(2000).
-!- FUNCTION: Peptide chain release factor 1 directs the termination of translation in response to the peptide chain termination codons of translation in response to the peptide chain termination codons UAG and UAA (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE PROKARYOTIC AND MITOCHONDRIAL RELEASE
                                                                                                    MEDLINE-20150912; PubMed-10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quall M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
             Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE-97061201; Pubmed-8905231;

Kanevo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Miyajima N., Mirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Okoundi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,

Okumura S., Shimpo S., Tabatuchi C., Wada T., Watanabe A.,

Yamada M., Yasuda M., Tabata S.,

Sequence analysis of the genome of the unicellular cyanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52; DB 1; Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 647F0202CB20B1B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 KMFEELKSRLDT-----LAQEVALLKEQQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
11-NOV-2002 (Rel. 41, Last annotation update)
Hypothetical protein s111433.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.2%; Score ...,
36.8%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                524 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRPAMS; TIGR00019; prfA; 1.
PROSITE; PS00745; RF_PROK_I; 1.
Protein blosynthesis; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR005139; PCRF.
InterPro; IPR000352; Pep_rel_factor_I.
InterPro; IPR004373; PrfA.
Pfam; PF00472; RF-1; I.
Pfam; PF03462; PCRF; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechocystis sp. (strain PCC 6803).
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL139079; CAB73600.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39943 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                          FACTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                              SEQUENCE FROM N.A. STRAIN-NCTC 11168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-1148;
                                                   NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YE33_SYNY3
P74217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93096045; PubMed-1461283;
Tinsley J.M., Blake D.J., Roche A., Fairbrother U., Riss J.,
Byth B.C., Knight A.E., Kendrick-Jones J., Suthers G.K., Love D.R.,
Edwards Y.H., Davies K.E.,
"Primary structure of dystrophin-related protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 31-256.
MEDLINE=20113481; Pubmed=10647184;
MEDLINE=20113481; Valuder S.J., Moores C.A., Walke S., Norwood F.L.M.,
Kendrick-Jones J.;
"Crystal structure of the actin-binding region of utrophin reveals head-to-tail dimer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Structure 7:1539-1546(1999).
-!- FUNCTION: MAY PLAY A ROLE IN ANCHORING THE CYTOSKELETON TO THE PLASMA MEMBRANE (BY SIMILARITY TO DYSTROPHIN).
-!- SUBCELLULAR LOCATION: NEUROMUSCULAR JUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostom1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 52; DB 1; Length 524;
Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Complete proteome,
SEQUENCE 524 AA; 55225 MW; 7E1527990b4133D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Utrophin (Dystrophin-related protein 1) (DRP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99141377; PubMed-9887274;
Keep N.H., Norwood F.L.M., Moores C.A., Winder S.J.,
Kendrick-Jones J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 144-261.
                                                                    DNA Res. 3:109-136(1996).
-!- SIMILARITY: BELONGS TO THE UPF0031 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 3433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D90913; BAA18311.1; -.
InterPro; IPR000631; UPF0031.
InterPro; IPR004643; YdeF_Nterm.
Ffam; PP01256; UPF0031; 1.
TIGRFAMS; TIGR0196; YjeF_cterm; 1.
TGRFAMS; TIGR0199; YjeF_nterm; 1.
PROSITE; PS01049; UPF0031_1; 1.
PROSITE; PS01049; UPF0031_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 360:591-593(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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NCBI_TaxID=5141;
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2045
2195
3193
3423
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                                                                                                                                                 DYHC_NEUCR
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NP_BIND
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                                                                                                        between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                           R PRINTS; PRO0403; Za, I. S. MANDOMAIN.

R SMART; SM00103; CH; 2.

R SMART; SM0013; CH; 2.

R SMART; SM00139; TarH; 1.

R SMART; SM00456; WW; 1.

R SMART; SM00199; ZarH; 1.

R PROSITE; PS00019; ACTININ_2; 1.

R PROSITE; PS01021; CH; 2.

R PROSITE; PS01159; WW_DOMAIN_1; 1.

R PROSITE; PS01159; WW_DOMAIN_1; 1.

R PROSITE; PS01159; WW_DOMAIN_2; 1.

R PROSITE; PS01159; WW_DOMAIN_2; 1.

R PROSITE; PS01159; Ze_Z=1; 1.

R PROSITE; PS01159; Ze_Z=2; 1.
        -:- SIMILARITY: STRONG, TO DYSTROPHIN.
-:- SIMILARITY: STRONG, TO DYSTROPHIN.
-:- SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIMBRIN, ABP-120, ABP-180, OR BETA-FODRIN).
-:- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
-:- SIMILARITY: CONTAINS 1 WA DOMAIN.
-:- SIMILARITY: CONTAINS 1 S2 SPECTRIN REPEATS.
-:- SIMILARITY: CONTAINS 1 Z2-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECTRIN 1.
SPECTRIN 2.
SPECTRIN 3.
SPECTRIN 4.
SPECTRIN 6.
SPECTRIN 6.
SPECTRIN 7.
SPECTRIN 7.
SPECTRIN 9.
                                                                                                                                                                                                                                   InterPro; IPR001589; Actbind_actnin.
InterPro; IPR001715; Calponin-like.
InterPro; IPR001715; Spectrin.
InterPro; IPR003122; TarH.
InterPro; IPR002349; WW.
InterPro; IPR001349; WW.Rap5_WWP.
InterPro; IPR0001303; WW.Rap5_WWP.
InterPro; IPR000433; Znf_ZZ.
Pfam; PF00307; CH; 2.
Pfam; PF00307; WW; 1.
Pfam; PF00305; Spectrin; 19.
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  TISSUE SPECIFICITY: MUSCLE.
                                                                                                                                                                              EMBL; X69086; CAA48829.1; -.
                                                                                                                                                                                                                    HGNC:12635; UTRN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1968
                                                                                                                                                                                       PIR; S28381, S28381.
PDB; 1BHD; 16-FEB-99.
PDB; 1QAG; 01-JAN-00.
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                                                                                                                                                                                                                             MIM; 128240;
                                                                                                                                                                                                                     Genew;
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COILED COIL (POTENTIAL).
ATP (POTENTIAL).
                                                                                               10;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 4367;
                                                         Length 3433;
                                                                                               Indels
                  3433 AA; 394488 MW; EAE8DB409F858E5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  iE10F3E2D170D6DF CRC64;
                                                                        Best Local Similarity 27.0%; Pred. No. 2.4e+02;
Matches 10; Conservative 12; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51.5; DB 1;
Pred. No. 3.6e+02;
                                                                                                                                                               :|| ::|: |:|
1895 LNTAIYEDFSFQEDSLKNIKDQLDKLGEQIAVIHEKQ 1931
                                                       30.2%; Score 52; DB 1;
                                                                                                                                      2 VNTKMFEE------LKSRLDTLAQEVALLKEQQ 28
                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                Dynein heavy chain, cytosolic (DYHC).
ZZ-TYPE
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InterPro; IPR004273; Dynein_heavy.
Pfam; PF03028; Dynein_heavy; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.9%;
50.0%;
                                                                                                                                                                                                                                                                               STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=74-OR23-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                         Neurospora crassa.
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RADIOLNE-20057165; Pubmed-10591208;
RA MEDLINE-20057165; Pubmed-10591208;
RA Clamp M. Sanik L.J. Aniscough R., Almeida J.P., Babbage A.K.,
RA Bagguley C., Balakey J., Barlow K.P., Bates K.N., Beasley O.P.,
RA Bagguley C., Balakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Bagguley C., Balakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chon Y., Clark G.,
RA Conroy D., Corbley N.E., Colle C.G., Cox A.V., Davis J., Dawson E.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhami P.D., Dookree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Gilbert J.G.R., Goward M.E., Garner A.A.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Hollmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Klmberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversia M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Washreqhi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Martyn I.D., Washreqhi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Martyn I.D., Washreqhi-Mohammadi M.A., Matthews L.H., Mccann O.T.,
RA Allilps S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Wilmig L.,
RA Williams C., Williams C., Williamson H., Willey D.L.,
RA Williams C., Williamson H., Williams C., Williams S., Rober S
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDIATE-91140735; PubMed-1847461; MEDIATE-91140735; PubMed-1847461; Traujimoto A., Nyunoya H., Morita T., Sato T., Shimotohno K.; Isolation of cDNAs for DNA-binding proteins which specifically bind to a tax-responsive enhancer element in the long terminal repeat of human T-cell leukemia virus type I."; J. Virol. 65:1420-1426(1991).
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Karpinski B.A., Morle G.D., Huggenvik J., Uhler M.D., Leiden J.M.; "Molecular cloning of human CREB-2: an ATF/CREB transcription factor that can negatively regulate transcription from the cAMP response
                                                                                                                                                                ATF4_HUMAN STANDARD; PRT; 351 AA.
P18848; Q9UH31;
01-NOV-1990 (Rel. 16, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2007 (Rel. 41, Last annotation update)
15-JUN-2007 (Rel. 41, Last annotation update)
15-JUN-2008 (Rel. 41, Last annotation update)
15-JUN-2008 (Rel. 41, Last annotation update)
16-JUN-2008 (Rel. 41, Last annotation update)
17-JUN-2008 (Rel. 41, Last annotation update)
18-JUN-2008 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
    ;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 89:4820-4824(1992),
5; Mismatches
                                                        3414 YAEILDRVGPLREEVMLL-EEQALQT 3438
                                  7 FEELKSRLDTLAQEVALLKEQQALQT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-92279218; PubMed-1534408;
Conservative
                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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13;
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Matches
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Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T., Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J., Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L., McDernid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L., Seroussi E., Fransson A., Wong A.C.C., Morrow B.E., Edelmann L., Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Wilkinson P., Boddenteich A., Hattman K., Hu X., Khan A.S., Lane L., Tibahun Y., Wright H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 274-341 FROM N.A.
MEDLINE=90185187; PubMed=2516827;
Hai T., Liu F., Coukos W.J., Green M.R.;
"Transcription factor ATF cDNA clones: an extensive family of leucine zipper proteins able to selectively form DNA-binding heterodimers.";
Genes Dev. 3:2083-2090(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE) (CONSENSUS: 5'GTGACGT(A/C)(A/G)-3'), A SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS.
-!- SUBUNIT: BINDS DNA AS A DIMER.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE BIIP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription regulation; DNA-binding; Activator; Nuclear protein. DNA_BIND 280 300 BASIC MOTIF. DOMAIN 306 334 LEUCINE-ZIPPER (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hai T., Liu F., Coukos W.J., Green M.R.;
Genes Dev. 4:682-6821990).
-!- FUNCTION: THIS PROTEIN BINDS TO A TAX-RESPONSIVE ENHANCER
ELEMENT IN THE LONG TERMINAL REPEAT OF HUMAN T-CELL LEUKEMIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE-Lung, and Placenta; Strausberg R.; Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P -> Q (IN REF. 3).
K -> R (IN REF. 2).
T -> R (IN REF. 5).
KEI -> REK (IN REF. 5).
I -> L (IN REF. 5).
X; 7A708C5CCD6ED7F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL022312; CAB45284.1; --
EMBL; BC008090; AAH08090.1; --
EMBL; BC011994; AAH11994.1; --
EMBL; BC024775; AAH24775.1; --
PIR; D34223; D34223.
TRANSFAC; T01303; --
Genew; HGNC:786; ATF4.
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PROSITE; PS00036; BZIP_BASIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004827; TF_bZIP. Pfam; PF00170; bZIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38558 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D90209; BAA14234.1; -. EMBL; M86842; AAA52071.1; -.
                                                                                                                                                                                                                                                                                                                          Nature 402:489-495(1999).
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339
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351 AA;
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VIRUS TYPE I
-!- FUNCTION: TH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 604064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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5 KMFEELKSRLDTLAQEVALLKE 26

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                             Kawashima T., Amano N., Kolke H., Makino S.-I., Higuchi S.,
Kawashima T., Amano N., Kolke H., Makino S.-I., Higuchi S.,
Kawashima Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
Archaeal adaptation to higher temepratures revealed by genomic sequence of Thermoplasma volcanium.";
Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000)

-! FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent coulcies as activity.
Rad50 provides an ATP-dependent control of mrell by unwinding and/or repositioning DNA ends into the mrell active site (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA repair; Hydrolase; ATP-binding; Colled coil; Complete proteome. 30 37 ATP (BY SIMILARITY). DOMAIN 17 77 COLLED COIL (POTENTIAL). SEQUENCE 895 AA; 103223 MW; 4A47DA9287E82D3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
--- SUBUNIT: Forms a complex with mrell (By similarity).
--- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
                                                                                                                                                                                                                                                                                        Archaeā; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.7%; Score 51; DB 1; Length 895; 40.0%; Pred. No. 81; ive 6; Mismatches 9; Indels
                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
MAD double-strand break repair rad50 ATPase.
RAD50 OR TV0228 OR TVG0235331.
                                                                                                                      895 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP000991; BAB59370.1; -.
INLECTPO; IPR003439; ABC_transportr.
InterPro; IPR003395; SMC_N.
Pfam; PF02463; SMC_N; I.
                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-GSS1 / DSM 4299 / JCM 9571;
MEDLINE-20570466; PubMed=11121031;
315 KKNEALKERADSLAKEIQYLKD 336
                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 40.0°
Matches 10; Conservative
                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                       Thermoplasma volcanium.
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=50339
                                                                                                                                                                                16-OCT-2001
                                                                                                                      RA50_THEVO
P58302;
                                                                                                   RA50_THEVO
                                                                             RESULT 15
```

Search completed: April 15, 2003, 11:48:30 Job time: 8.5 secs

202 NNKQIEELESKLRLIEPEIKALEEE 226

q ò

3 NTKMFEELKSRLDTLAQEVALLKEQ 27

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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 protein search, using sw model OM protein April 15, 2003, 11:45:44; Search time 11.75 Seconds (without alignments) 294.540 Million cell updates/sec Run on:

US-09-445-576A-36 Title: Perfect score:

172 1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues Searched:

283224

seq length: 0 seq length: 2000000000 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ď			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	. Description
	172	100.0	202	-	TTHUN	tetranectin precur
7	146	84.9	202	7	JC4031	tetranectin precur
Э	84	48.8	166	٦	A37289	
4	09	34.9	761	7	T03719	>
S	58	33.7	853	7	T51505	hypothetical prote
9	57.5	33.4	279	7	JC5403	
7	57	33.1	307	~	AE0962	E
œ	57	33.1	311	7	A65010	D-serine deaminase
σ	'n	32.6	425	7	н83652	seryl-tRNA synthet
10	55.5		252	~	T24939	hypothetical prote
11	52	32.0	486	~	B84914	hypothetical prote
12	'n	31.4	126	7	B70575	~
13	53.5	31.1	381	7	A54415	
14	53	30.8	197	7	F64474	· hypothetical prote
15		30.8	222	7	G97129	_
16	53	30.8	374	7	D70391	_
17	53	30.8	380	7	H83994	
18	53	30.8	616	7	S54389	NCA2 protein - yea
19	53	30.8	1034	7	AB0551	S
20	53	30.8	1043	7	T51228	hypothetical prote
21	53		1549	7	T21809	hypothetical prote
22	52.5		275	7	S25816	ribosomal protein
23	ά.	30.5	323	7	T07734	homeotic protein V
24	52		355	7	B81257	translation releas
25	52		524	7	S75852	hypothetical prote
	52	30.5	857	7	F81396	ATP-dependent CLP
27	52	30.5	1178	7	S54073	probable membrane
28	52	30.5	1356	7	-	pre
58	52	30.2	3433	_	S28381	utrophin - human

dynein heavy chain	transcription fact	conserved hypothet	two-component sens	Na+/K+-exchanging	probable myosin he	early endosome ant	hypothetical prote	conserved hypothet	hypothetical prote	probable membrane	serine O-acetyltra	hypothetical prote	conserved hypothet	hypothetical membr	embryogenic callus
B54802	A45377	AI0458	G83990	B37227	F84730	A57013	S38011	AE0012	T13518	826809	875606	C59107	F86714	B82931	T14286
	7	~	7	7	7	7	7	7	7	~	7	7	~	7	7
4367	351	498	597	1010	1269	1410	619	79	181	224	249	349	369	394	502
29.9	29.7	29.7	29.7	29.7	29.7	29.7	29.4	29.1	29.1	29.1	29.1	29.1	29.1	29.1	29.1
51.5	51	51	51	51	51	51	50.5	20	20	20	20	20	20	20	20
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
A;Cross-references: EMBL:X70911
R;Wewer, U.M.; Albrechtsen, R.
Lab. Invest. 67, 253-262, 1992
A;Title: Tetranectin, a plasminogen kringle 4-binding protein. Cloning and gene expre
A;Reference number: A56835; MUID:92365345; PMID:1354271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X64559; NID:937408; PIDN:CAA45860.1; PID:937409
A;Experimental source: placenta
R;Fublendorff, J.; Clemmensen, I.; Magnusson, S.
Biochemistry 26, 6757-6764, 1987
A;Title: Primary structure of tetranectin, a plasminogen kringle 4 binding plasma pro A;Reference number: A29747; MUID:88107595; PMID:3427041
tetranectin precursor [validated] - human N;Alternate names: plasminogen-kringle 4 binding protein C;Species: Homo sapiens (man) C;Dactes 30-Jun-1992 #sequence_revision 03-Aug-1995 #text_change 08-Dec-2000 C;Accession: S24126; A56835; A29747; I38359; S19865 R;Berglund, L.; Petersen, T.E. FEBS Lett. 309, 15-19, 1992
                                                                                                                                                                                                                                                               A;Title: The gene structure of tetranectin, a plasminogen binding protein. A;Reference number: S24126; MUID:92380263; PMID:1511740
A;Accession: S24126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F.1-21/Domain: signal sequence #status predicted <SIG>
F.12-202/Product: tetranectin #status experimental <MAT>
F.72-202/Product: tetranectin #status experimental <MAT>
F.71-197/Domain: C-type lectin homology <LCHP:
F.75/Binding site: carbobydrate (Thr) (covalent) #status experimental
F.71-81,98-197,173-189/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 172; DB 1;
100.0%; Pred. No. 1.2e-13;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: tetranectin; C-type lectin homology C;Keywords: glycoprotein; plasma; tetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GDB:135032; OMIM:187520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 22-105, 'G', 107-202 <FUH>
A; Experimental source: plasma
A; Note: 55-5cr and 58-Met were also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 100.0
Best Local Similarity 100.0
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 3p22-3p21.3
A; Introns: 37/1; 70/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Complex: homotetramer
                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-202 <BER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-202 <WEW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB:TNA
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1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36

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Gaps

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Indels

ij

Gaps

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Indels

12;

Length 761;

DB 2;

S.

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hypothetical 32.1K protein - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: 07-Jul-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jun-2000
C;Accession: JG5403
R;Nambiar, A.; Kandala, J.C.; Dolan, S.A.; Jensen, J.B.; Guntaka, R.V.
R;Nambiar, A.; Kandala, J.C.; Dolan, S.A.; Jensen, J.B.; Guntaka, R.V.
A;Tille: Molecular cloning and characterization of a cDNA for the highly conserved HM A;Reference number: JG5403; MUID:97312528; PMID:9168969
A;Accession: JG5403
A;Molecule type: mRNA
A;Residues: 1-279 <NAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. Species: Arabidopsis thalian and acceptances)
C. Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C. Accession: T51505
S. Nakamura, T.: Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S. Submitted to the Protein Sequence Database, August 2000
A. Reference number: 225394
A. Accession: T51505
A. Status: preliminary
A. Molecule type: DNA
A. Residues: 1-853 < SAT>
A. Cross-references: EMBL:AL391147
A. Experimental source: cultivar Columbia; BAC clone F5E19
C. Genetics:
                                                                                           NID:92618824; PIDN:AAB84386.1; PID:92618825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D-serine deaminase activator [imported] - Salmonella enterica subsp. enteric
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C;Accession: AE0962
                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F5E19_70 - Arabidopsis thaliana
              translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58; DB
Pred. No. 35;
4; Mismatches
                                                                                                                                                                         Pred. No. 18;
5; Mismatches
                                                                                                                                                                                                                                                            2 VNTKMFEELKSRLDTLAQEVALLKE--QQALQTV 33
                                                                                                                                                                                                                                                                                               12 VNSNQFEELLQERDKLKQQVKKMEEWKQQVMTTV 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 57.5;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 NTKMFEELKSRLDTLAQEV -- ALLKEQQALQTV 33
                                                                                                                                                     Score 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 NTSNFENIKSTIESTNCDEIALLKDKDA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29
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                                                                                           A; Cross-references: EMBL: AF011368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.7%;
48.5%;
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                                                                                                                                                  Query Match 34.9%;
Best Local Similarity 44.1%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 33.79
Best Local Similarity 48.55
Matches 16; Conservative
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Best Local Similarity
Matches 13; Conserv
                                     A; Molecule type: mRNA
A; Residues: 1-761 <ABE>
              preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 5
A; Introns: 6/2; 79/3
A; Note: F5E19_70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tetranectin homolog - reef shark
C;Species: Carcharhinus springeri (reef shark)
C;Species: Carcharhinus springeri (reef shark)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A37289; A37287
R;Neame, P.J.; Young, C.N.; Treep, J.T.
R;Neame, P.J.; Young, C.N.; Treep, J.T.
A;Title: Primary structure of a protein isolated from reef shark Carcharhinus springeri
A;Reference number: A37289; MUID:93284081; PMID:1304877
A;Accession: A37289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene CEV1
                                                                                                                                                                                                                                                                                                                                                                                                               A.Molecule type: mRNA
A.Residues: 1-202 <SOR>
A.Cross-references: BMBL.X79199; NID:g671561; PIDN:CAA55791.1; PID:g671562
A.Experimental source: lung
C.Comment: This protein binds plasminogen, and may play a role in invasive cancer.
C.Superfamily: tetranectin; C-type lectin homology
C.Superfamil: signal sequence #status predicted <SIS>
F:1-21/Domain: signal sequence #status predicted <MAT>
F:22-202/Product: tetranectin #status predicted <MAT>
F:71-197/Domain: C-type lectin homology <LCH>
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0
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Blood 90, 4271-4277, 1997
A;Title: Fusion of the platelet-derived growth factor receptor beta to a novel
A;Reference number: Z15027; MUID:98043615; PMID:9373237
                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 20-Aug-1999
C;Accession: JC4031
R;Sorensen, C.B.; Berglund, L.; Petersen, T.E.
Gene 152, 243-245, 1995
A;Title: Cloning of a cDNA encoding murine tetranectin.
A;Reference number: JC4031; MUID:95137396; PMID:7835708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable thyroid receptor interactor - human (fragment)
N;Alternate names: CEV14 protein
C;Species: Homo sapiens (man)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 08-Oct-1999
C;Accession: T03719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;37-160/Domain: C-type lectin homology <LCH>F;37-47,64-160,136-152/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.9%; Score 146; DB 2;
80.6%; Pred. No. 1.7e-10;
tive 6; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
0.0045;
Superfamily: tetranectin; C-type lectin homology:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 LVSSKMFEELKNRMDVLAQEVALLKEKQALQTVCLK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
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48.8%; Score 84; DB
Best Local Similarity 58.6%; Pred. No. 0.00
Matches 17; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EELKSRLDTLAQEVALLKEQQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity, 80.07
                                                                                                                                                                      tetranectin precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 1-166 <NE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Keywords: cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: T03719
                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: JC4031
                         38
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Length 279;

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Gaps

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Indels

Length 425;

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hypothetical protein At2947350 [imported] - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C; Accession: B84914 S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujli, C.Y R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-252 <WILD
A; Cross-references: EMBL:247356; PIDN:CAA87415.1; GSPDB:GN00020; CESP:T15H9.2
A; Experimental source: clone T15H9
C; Genetics:
A; Gene: CESP:T15H9.2
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A;Cross-references: GB:AE002093; NID:92275213; PIDN:AAB63835.1; GSPDB:GN00139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T15H9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24939
R;Gardner, A.
Submitted to the EMBL Data Library, January 1995
A;Reference number: 219958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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A;Molecule type: DNA
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                                                                                                                   ore 56; DB;
ed. No. 30;
Mismatches
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Pred. No. 45;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
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Pred. No. 20
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                                                                                                                   Score 56;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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A;Introns: 29/3; 70/1; 95/1; 131/2; 178/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 EQLKSQLSRLDSSVAILKSQQMAVKSV 147
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                                                                                                                                                                                                          5;
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EELKSRRNQVSQEVAQLKREK 66
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40.6%;
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51.9%;
                            C; Superfamily: serine-tRNA ligase
                                                                                                                   32.6%;
ilarity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                     8 EELKSRLDTLAQEVALLKEQO
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Best Local Similarity 51.9'
Matches 14; Conservative
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Best Local Similarity 40.6
Matches 13; Conservative
                                                                                                                   Query Match
Best Local Similarity
Matches 12; Conserv
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A;Map position: 2
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B70575
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B84914
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C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: #83652
C;Accession: #83652
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirra
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-425 <GTO>
A;Cross-references: GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BAB03743.1; GSPDB:GNOC
C;Genetics:
A;Gene: serS
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Arither complete genome sequence of a multiple drug resistant Salmonella enterica serow A:Reference number: AB0502; PMID:11677608
A:Accession: AE0962
A:Status: prealiminary
A:Residues: 1-307 <PAR>
A:Residues: 1-308 <PAR>
A:Residues: 1-308 <PAR}
A:Residues: 1-308
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A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: A65010
A:Accession: A65010
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Residues: 1-311 <BLAT>
A:Residues: 1-311 <BLAT>
A:Cross references: GB:AE000324; GB:U00096; NID:g1788694; PIDN:AAC75423.1; PID:g1788706; G:Genetics: Strain K-12, substrain MG1655
C;Genetics: A:Gene: dsdC
C;Superfamily: regulatory protein ampR
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C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: A65010
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
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Pred. No. 16;
6; Mismatches
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77 RVYWALKSSLDTLNQEILDIKNQELSGTLTL 107
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ilarity 44.8%;
Conservative
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Matches 13; Conserva
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Length 252;

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Length 197 Indels

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hypothetical protein CAC1862 [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Acession: G97129
R; Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L. J. Baly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J; Balty, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J; Bacteriol. 183, 4823, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Accession: G97129
A; Accession: G97129
A; Residues: 1-22 <KUR>
                                        A:Cross-references: GB:U67580; GB:L77117; NID:g1592044; PIDN:AAB99408.1; PID:g1592047 C.Scenetics: A:Map posttion: REV13593931-1359338 C:Superfamily: hypothetical protein MJ1399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB:AE001437; PIDN:AAK79826.1; PID:915024839; GSPDB:GN00168
A; Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.8%; Score 53; DB 2; Length 222; 37.8%; Pred. No. 35; 1ve 5; Mismatches 11; Indels
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                                                                                                                                                                                                           Ouery Match 30.8%; Score 53; DB Best Local Similarity 47.6%; Pred. No. 31; Matches 10; Conservative 5; Mismatches
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He : 13.75 secs
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Matches 17; Conservative
             A; Residues: 1-197 <BUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: CAC1862
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C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 21-Jul-2000
C;Accession: A54415; #sequence_revision 07-Jul-1995 #text_change 21-Jul-2000
C;Accession: A54415; #sequence_revision 07-Jul-1995 #text_change 21-Jul-2000
R;Mikami, K.; Sakamoto, A.; Iwabuchi, M.
J. Biol. Chem. 269, 9974-9985, 1994
J. Biol. Chem. 269, 9974-9985, 1994
A;Title: The HBP-1 family of Wheat basic/leucine zipper proteins interacts with overlapp A;Reference number: A54415; MUID:94193693; PMID:8144592
                                                                                        Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Holroyd, S. Nature 393, 537-544, 1998
A:Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-126 <COL>
A;Cross-references: GB:Z95324; GB:AL123456; NID:g3261760; PIDN:CAB08585.1; PID:g2094832
A;Experimental source: strain H37Rv
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: F64474
R; Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R; Reich, C.J.; White, O.; Okrbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; A; Itle: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A; Reference number: A64300; MUID: 96337999; PMID: 8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:D12920; NID:95926680; PIDN:BAA02304.1; PID:9497895
C;Superfamily: fava bean G-box-binding protein; fos/jun DNA-binding domain homology
C;Keywords: DNA binding; transcription factor
F;297-337/Domain: fos/jun DNA-binding domain homology <FJD>
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul_1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein MJ1399 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep_1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
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44.0%; Pred. No. 15;
tive 6; Mismatches
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Pred. No. 53;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: hspR
C;Superfamily: probable heat shock protein merR
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A;Molecule type: mRNA
A;Residues: 1-381 <MIK>
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Best Local Similarity
                                                                C; Accession: B70575
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein April 15, 2003, 11:48:39; Search time 23:25 Seconds Run on:

(without alignments)
241.276 Million cell updates/sec

US-09-445-576A-36

172 1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK Perfect score: Sequence:

36

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

704857 segs, 155824263 residues Searched:

704857 Total number of hits satisfying chosen parameters:

Minimum DB : Maximum DB :

seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Pending_Patents_AA_New:*

| cgn12_6/ptodate1/2/paa/PCT_NEW_COMB.pep:*
| cgn12_6/ptodate1/2/paa/US06_NEW_COMB.pep:*
| cgn12_6/ptodate1/2/paa/US07_NEW_COMB.pep:*
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| cgn12_6/ptodate1/2/paa/US09_NEW_COMB.pep:*
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| cgn12_6/ptodate1/2/paa/US00_NEW_COMB.pep:*
| cgn12_6/ptodate1/2/paa/US00_NEW_COMB.pep:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

6, Appli 26, Appl Appl App1 Sequence 36, App] Description Sequence US-09-513-999C-4342 US-09-445-576A-39 US-09-445-576A-38 PCT-US02-19669A-55 US-09-99-50-62 US-09-999-570-62 US-10-154-678-62 US-10-276-781-1559 US-09-445-576A-24 US-09-445-576A-28 US-09-445-576A-28 US-09-445-576A-26 US-09-445-576A-26 US-09-445-576A-26 US-09-445-576A-26 US-09-445-576A-26 US-09-445-576A-31 US-09-445-576A-32 US-09-445-576A-33 US-09-445-576A-34 US-09-445-576A-25 PCT-US02-38407-13 US-09-445-576A-27 US-09-445-576A-7 DB Length Query Match 1 Score Result š

1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36

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Sequence

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557, AF 403, P 403, P 403, P 5276, P 5			Gaps		Gaps
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			Length 36, Indels		Length 52, Indels
27 75 43.6 206 1 PCT-US02-19669A-57 28 75 43.6 206 5 US-09-992-733-403 30 75 43.6 206 6 US-09-992-643-403 31 75 43.6 206 6 US-10-125-923A-276 33 75 43.6 206 6 US-10-125-923A-276 34 75 43.6 206 6 US-10-125-923A-276 34 75 43.6 206 6 US-10-14-575-276 35 75 43.6 206 6 US-10-14-575-276 35 75 43.6 206 6 US-10-187-75-276 37 75 43.6 206 6 US-10-199-67-276 37 75 43.6 206 6 US-10-199-67-276 38 64 37.2 36 105-10-199-67-276 76 39 60 34.9 7 105-09-949-016-7404 70	ALIGNMENTS	RESULT 1 US-09-445-576A.36 US-09-445-576A.36 Sequence 36, Application US/09445576A Sequence 36, Application US/09445576A SEQUENCE INFORMATION: APPLICANT: BOREAN PARMA A/S TITLE REFERENCE: 62032.000004 CURRENT APPLICATION NUMBER: US/09/445,576A CURRENT FILING DATE: 2000-07-17 NUMBER OF SEQ ID NOS: 104 SEQ ID NO 36 LENGTH: 36 TYPE: PATE OF SEQ ID NOS: 104 SEQ ID NO 36 USEQ ID NO	Query Match 100.0%; Score 172; DB 5; Best Local Similarity 100.0%; Pred. No. 4.4e-18; Matches 36; Conservative 0; Mismatches 0; Qy 1 VVNTKMFEELKSRLDTLAQEVALLKEQOALQTVCLK 36	SULT 2 -09-445-576A-71 Sequence 71, Application US/09445576A SEMERAL INFORMATION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE REPERENCE: 6203.00000, TURRENT APPLICATION NUMBER: US/09/445,576A CURRENT FILING DATE: 2000-07-17 NUMBER OF SEQ ID NOS: 104 SOFTWARE: Patentin version 3.1 LENGTH: 52 TYPE: PRT TYPE: PRT O-09-445-576A-71	Query Match 100.0%; Score 172; DB 5; Best Local Similarity 100.0%; Pred. No. 7e-18; Matches 36; Conservative 0; Mismatches 0;

Gaps

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FORT-USO2-38407-13
Sequence 13, Application PC/TUSO238407
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: OSTEOARTHRITIS
TITLE OF INVENTION: OSTEOARTHRITIS
TITLE OF INVENTION: OSTEOARTHRITIS
TILE REPERENCE: D0189
CURRENT APPLICATION NUMBER: PCT/USO2/38407
CURRENT FILING DATE: 2002-12-03
PRIOR PPLICATION NUMBER: 60/337,417
PRIOR FILING DATE: 2001-12-03
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TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.055.DIV
CURRENT APPLICATION NUMBER: US/09/992,095B
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                       Indels
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3.8e-17;
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100.0%; Score 172; DB 5;
Best Local Similarity 100.0%; Pred. No. 3.7e-17;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                        1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
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PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR PLICATION NUMBER: PCT/IB01/01715
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 112
SSOFTWARE: JPatent
LENGTH: 202
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GENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
                       ; FEATURE:
; OTHER INFORMATION: H6FXTN123
US-09-445-576A-25
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ORGANISM: Homo Sapiens
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ORGANISM: Homo sapiens
  ORGANISM: Artificial
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LENGTH: 202
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Pred. No. 3.3e-17;
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100.0%; Score 172; DB 5;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0;
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                                                                                                                                                            APPLICANT: Borean Pharma A/S
IITLE OF INVENTION: Trimerising module
FILE REFERENCE: 62032 000004
CURRENT APPLICATION NUMBER: US/09/445,576A
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
LENGTH: 180
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TITLE OF INVEWTION: Tringerising module
FILE REPERENCE: 62032.000004
CURRENT APPLICATION NUMBER: US/09/445,576A
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.1
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TITLE OF INVENTION: Trimerising module
FILE REFERENCE: 62032.000004
CURRENT APPLICATION NUMBER: US/09/445,576A
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.1
                                                                     RESULT 3
US-09-445-576A-27
Sequence 27, Application US/09445576A
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; P

Matches 36; Conservative 0;
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US-09-445-576A-27
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LENGTH: 181
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, inc.
APPLICANT: Application of al.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-018 (785 contig)
CURRENT FILING DATE: 2002-11-18
PRIOR PELING DATE: 2002-11-18
PRIOR FILING DATE: 2000-01-25
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100.0%; Score 172; DB 5;
Best Local Similarity 100.0%; Pred. No. 4.4e-17;
Matches 36; Conservative 0; Mismatches 0;
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100.0%; Score 172; DB 6;
Best Local Similarity 100.0%; Pred. No. 3.8e-17;
Matches 36; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: Trimerising module
FILE REFERENCE: 62032.000004.
CURRENT APPLICATION NUMBER: US/09/445,576A
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 104
SEQ ID NO 24
LENGTH: 228
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1559
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US-09-445-576A-24
  PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARE: JPatent
                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-276-781-1559
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                                                                                                                                                                               ; NAME/KEY: SIGNAL
; LOCATION: -21..-1
US-10-154-678-62
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US-10-276-781-1559
                                            SOFTWARE: JPat
SEQ ID NO 62
LENGTH: 202
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FILLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 6-0910308D1V
CURRENT APPLICATION NUMBER: 2001-06-14
PRIOR PELICATION NUMBER: US 09/924,340
PRIOR PELICATION NUMBER: US 09/924,340
PRIOR PELICATION NUMBER: PCT/IBO1/01715
PRIOR APPLICATION NUMBER: PCT/IBO1/01715
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
SOFTWARE: JPATENT
SEQ ID NO 62
FENNMBER OF SEQ ID NOS: 112
FENNMBER OF SEQ ID NOS: 112
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TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 182.051.REG
CURRENT APPLICATION NUMBER: US/10/154,678
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 69/924,340
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR PILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-29
PRIOR PLING DATE: 2001-06-29
PRIOR PLING DATE: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
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                                                               Query Match 100.0%; Score 172; DB 5; Best Local Similarity 100.0%; Pred. No. 3.8e-17; Matches 36; Conservative 0; Mismatches 0;
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Pred. No. 3.8e-17;
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1 Similarity 100.0%;
36; Conservative 0
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ORGANISM: Homo sapiens
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Best Local Similarity
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; LOCATION: 1..21
US-09-999-570-62
; LOCATION: 1..21
US-09-992-095B-62
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US-09-999-570-62
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US-10-154-678-62
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ORGANISM: Artificial
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; OTHER INFORMATION: tetranectin polypeptide sequence for Glul to Lys52
US-09-445-576A-5
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97.2%; Pred. No. 1.9e-16;
Live 0; Mismatches 1
1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
                    1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
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GENERAL INFORMATION:
APPLICANT: Borean Pharma A/S
TITLE OF INVENTION: Trimerising module
FILE REFERENCE: 62032.000004
CURRENT APPLICATION NUMBER: US/09/445,576A
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCL 35
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FILE REFERENCE: 62032.000004
CURRENT APPLICATION NUMBER: US/09/445,576A
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
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TITLE OF INVENTION: Trimerising module
FILE REFERENCE: 62032.00004
CURRENT APPLICATION NUMBER: US/09/445,576A
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.1
SQOTUMARE: 73
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; Sequence 28, Application US/09445576A
; GENERAL INFORMATION:
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Best Local Similarity 97.29
Matches 35; Conservative
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US-09-445-576A-35
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                                                                                                     US-09-445-576A-35
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US-09-445-576A-5
                                                                                                                                                                                                                                                                                                             TYPE: PRT
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TYPE: PRT
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                                                                                                       Gaps
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                                                             Length 73;
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                                                                                                   1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 89.5%; Score 154; DB 5; 18est Local Similarity 100.0%; Pred. No. 2.6e-15; Matches 33; Conservative 0; Mismatches 0;
                                                           DB 5;
                                                         Score 162; DB 5;
Pred. No. 3e-16;
0; Mismatches
                                                                                                                               1 VVNTKMFBELKSRLDTLAQEVALLKEQQALQTVCLK 36
                                                                                                                                                  1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTV 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTV 49
                                                                                                                                                                                                                                                                                               APPLICANT: Borean Pharma A/S
TITLE OF INVENTION: Trimerising module
FILE REFERENCE: 62032.000004
CURRENT APPLICATION NUMBER: US/09/445,576A
CURRENT FILING DATE: 2000-07-17
NUMBER OF SEQ ID NOS: 104
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: April 15, 2003, 12:05:47 Job time: 25.25 secs
                                                                                                                                                                                                                        RESULT 15
US-09-445-576A-6
Sequence 6, Application US/09445576A
GENERAL INFORMATION:
                                                       94.2%;
ilarity 97.2%;
Conservative
; OTHER INFORMATION: H6FXLripa
US-09-445-576A-28
                                               Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial
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April 15, 2003, 11:43:14 ; Search time 28.75 Seconds (without alignments) 166.853 Million cell updates/sec
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK
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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence:
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A_Geneseq_101002: Database

Listing first 45 summaries

Post-processing: Minimum Match 0% Maximum Match 100%

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*/SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1998.DAT:*/SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1999.DAT:*/SIDS2/gcgdata/geneseqy/geneseqp-embl/AA1999.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994_DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995_DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:* /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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/SIDSZ/gcgdata/geneseq/geneseqp-embl_AA1987.DAT:* 16: 17: 20:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	•		Description	H6FXTN23 fusion pr	Human tetranectin	H6FXTN123 fusion p	Human tetranectin.	Human EST encoded	CIIH6FXTN123 fusio	Sequence of chain	, Tetranectin polype	H6FXtripa fusion p	Tetranectin polype
SUMMARIES			ΙD	AAW94264	AAW94256	AAW94262	AAR60521	AAM24034	AAW94261	AAP60098	AAW94254	AAW94270	AAW94255
			DB	20	50	20	15	22	20	7	20	20	20
			Match Length DB ID	180	181	197	202	202	228	182	52	73	49
	æ	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	97.1	94.2	94.2	89.5
			Score	172	172	172	172	172	172	167	162	162	154
		Result	Q	-	7	М	4	2	9	7	80	6	10

H6FXTr1D fusion pr H6FXtr1pB-UB fusion p H6FXtr1pB-UB fusio H6FXscFv(CEA6)tr1p H6FXtr1pBscFv(CEA6) H6FXScFv(CEA6)tr1p H0Man secreted pro Protein encoded by Human breast tumou Membrane-bound pro Human PRO1958 enco Peptide #5060 enco Peptide #5168 enco Protein #5120 enco Protein #5120 enco Protein #5120 enco Protein #5120 enco Peptide #5068 enco Protein #5120 enco Protein #5120 enco Protein #5120 enco Protein #5120 enco Protein #5120 enco Protein #5120 enco Protein #5148 enco Peptide #5068 enco Schizophrenia-Asso Schizophrenia-Asso Schizophrenia-Asso Schizophrenia-Asso	C albicans apoptos Streptococcus poly Arabidopsis thalla Arabidopsis thalla Arabidopsis thalla Drosophila melanog
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111 1121 1132 1148 1158 1168 1178 1178 1178 1178 1178 1178 117	0 4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5
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ALIGNMENTS

RESULT 1

Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imagling; tumour; human; tetranectin; H6FXTN23. AAW94264 standard; protein; 180 AA H6FXTN23 fusion protein sequence. 98WO-DK00245 97DK-0000685 (first entry) (ETZE/) ETZERODT M. (GRAV/) GRAVERSEN N J H. (HOLT/) HOLTET T L. (KAST/) KASTRUP J S. WO9856906-A1. 26-APR-1999 Homo sapiens 11-JUN-1998; 11-JUN-1997; 17-DEC-1998. Synthetic. AAW94264; AAW94264

Kastrup JS;

Graversen NJH, Holtet TL, Nielsen BB, Thogersen HC;

Etzerodt M, Larsen IK, Kastrup JS;

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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein camily: The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural construct comprise at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologus construct complex with 2 other TSEs, with the proviso that the heterologus moiety is different from TTSEs, with the proviso that the heterologus moiety is different from any of the fusion proteins CIHGEXTN123, HGFXTN12, HGFXTN23 (AAM94261 to AAM94261). The TTSE can be used for the construction of structure, a toxin, a detectable label, an in situ activatable substance, an enzyme, a radioactive moiety, a cytokine, an on-proteinaceous polymer, andocross-linking agent, or a group facilitating conjugation of the photo cross-linking agent, or a group facilitating conjugation of the monomer polypeptide construct to a target. They can be used as vehicles of or assembling antibody fragments into oligomeric or multivalent constructs can be used for targeted gene therapy involving selective constructs can be used for transfection or infection of the specific population of cells. They can also be used for delivering a substance to a cell or tissue or for delivering an imaging or toxin-conjugated cat selective at the construct or a wide variety of conjugates. The present sequence constructs and wide variety of conjugates. The presents and second so act as a vehicle for a maiso be used for delivering a substance of act as a vehicle for a wide variety of conjugates. The present sequence represents a H6FXTN23 fusion protein sequence. The specification claims contains the heterologous moiety to which the TTSEs of the invention are consequence.
                                                                                 New monomer polypeptide constructs for diagnosis and therapy - comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
                                                                                                                                                                                                                                Disclosure; F19 8; 110pp; English.
                              WPI; 1999-080897/07
                                                                                                                                                                            activity
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.; Length 180; Indels 100.0%; Score 172; DB 20; 100.0%; Pred. No. 7.3e-14; 1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36 Mismatches ; 36; Conservative Local Similarity 180 AA; Sequence Query Match Matches Best ò

셤

AAW94256 standard; protein; 181 AA AAW94256; RESULT 2 AAW94256

26-APR-1999 (first entry)

Human tetranectin amino acid sequence.

Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin.

Homo sapiens.

WO9856906-A1.

17-DEC-1998.

98WO-DK00245. 11-JUN-1998;

The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous moiety, the TTSE being capable of forming a stable complex with 2 other TTSEs, with the proviso that the heterologous moiety is different from any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN12 (AAM94261 to AAM94264). The TTSE can be used for the construction of conjugates with heterologous moietys and still activatable substance, an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer, a photo cross-linking agent, or a group facilitating conjugation of the monomer polypeptide construct to a target. They can be used as vehicles for generating chimeric artificial antibodies having preselected pharmacokinetic and/or pharmadynamic properties. The constructs can be used for trangeted gene therapy involving selective delivery of the material for transfection or infection of the specific population of cells. They can also be used for delivering a substance to a cell or tissue or for delivering an imaging or transmiting and a religion or processed to a religion of the specific and a time of a religion or processed to a religion of the specific and a time of a religion or processed to a religion of the specific and a time of a religion or processed to a religion of the material or the mate antibody to a tumour. They can also be used for prevention or treating a disease or for diagnosis. The TTSE provides a stable structure which can act as a vehicle for a wide variety of conjugates. The present sequence represents a human tetranectin sequence from which the TTSE can be New monomer polypeptide constructs for diagnosis and therapy comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional activity 100.0%; Score 172; DB 20; 100.0%; Pred. No. 7.3e-14; 1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36 17 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 52 0; Mismatches Graversen NJH, Holtet TL, Thogersen HC; Claim 10; Page 60; 110pp; English. 97DK-0000685. Conservative J.H. Nielsen BB, (KAST/) KASTRUP J S. GRAVERSEN N WPI; 1999-080897/07 Best Local Similarity Matches 36; Conserv 181 AA; HOLTET 11-JUN-1997; Etzerodt M, Larsen IK, Sequence Query Match GRAV/ q ö Gaps

Trimeric polypeptide: tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; H6FXTN123. AAW94262 standard; protein; 197 AA H6FXTN123 fusion protein sequence. (first entry) 26-APR-1999 AAW94262; RESULT 3 AAW94262

Gaps

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Length 181; Indels

DB 20;

Homo sapiens

us-09-445-576a-36.rag

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cDNA encoding human tetranectin (full sequence given in AAR60521) was PCR amplified cDNA was linked to a sequence encoding the Factor-xa cleavage site (given in AAR60503), subcloned in vector pT7H6 so that it was linked to a hexabilistidine-encoding sequence and expressed in E. coli BL21. The fusion protein was purified on an Ni2+-activated WTR-agarose column. A cyclic procedure was used to obtain correctly folded recombinant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Refolding of polypeptide molecules - using a cyclic process involving denaturing and renaturing conditions to produce a correctly folded prod
                                                                      protease; Factor-Xa; recognition site; tetranectin; protein cleavage; protein folding; primer;
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100.0%; Pred. No. 8.3e-14;
iive 0; Mismatches 0;
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                                                                                                                            polymerase chain reaction; amplification
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93DK-0000139.
93WO-GB02492.
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Best Local Similarity 100.
Matches 36; Conservative
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                         Human tetranectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide
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comprise a tetranectin trimerising structural element covalently
linked to at least one heterologous moiety for providing functional
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tive 0; Mismatches (
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                                                                                                                         98WO-DK00245
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Nielsen BB, Th
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GRAVERSEN N J H.
                                                                                                                                                                                                                                                                                     HOLT/) HOLTET T L.
(KAST/) KASTRUP J S.
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nes 36; Conserv
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                WO9856906-A1
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                                                                      17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                       Etzerodt M,
                                                                                                                                                                                                                                                                                                                                                                                                   Larsen IK,
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activity

ETZE/) GRAV/) Seguence

Query Match

Matches

ò ద AAR60521;

EX Y X E

RESULT 4 AAR60521

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Gaps

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Indels

Length 202;

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228 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP206400-A.
                                         activity
                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP60098;
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                          sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP60098
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                                                                                                                                                                    The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat., horse, ow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                           Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytoxine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; CIIH6FXIN123.
                                                                                                                           polypeptide for treatment of diseases, diagnostics, raising
                                                                                                                                                                                                                                                                                             Gaps
                                                                           Asundi V;
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                                                                                                                                                                                                                                                                                            Indels
                                                                          Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kastrup JS;
                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                       100.0%; Score 172; DB 22; 100.0%; Pred. No. 8.3e-14;
                                                                       Zhou P, Qian XB, Wang Z,
V, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                        1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                   VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 73
                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Graversen NJH, Holtet TL,
Nielsen BB, Thogersen HC;
                                                                                                                                                   Claim 20; Page 1069; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         CIIH6FXTN123 fusion protein sequence.
                                                                                                                                                                                                                                                                                                                                                                         Ā
                                                                                                                                                                                                                                                                                                                                                                      AAW94261 standard; protein; 228
        2000US-0491404.
2000US-0617746.
2000US-0631451.
2000US-0663870.
                                                                                                                                     and research use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97DK-0000685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-DK00245
                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                           Best Local Similarity
watches 36; Conservative
                                                                                                                                                                                                                                    protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRAVERSEN N J H. HOLTET T L.
                                                                      , Liu C, Zh
Drmanac RA,
                                                                                                WPI; 2001-476164/51.
N-PSDB; AAH98693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KAST/) KASTRUP J S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-080897/07
                                                                                                                                                                                                                                                     202 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETZE/) ETZERODT M.
                                                     HYSE-) HYSEQ INC
                                     15-SEP-2000;
        25-JAN-2000;
17-JUL-2000;
                          03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                          26-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9856906-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUN-1997;
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                                                                                                                                    antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Larsen IK,
                                                                       ΥT,
                                                                                                                            Isolated
                                                                                                                                                                                                                                                                                                                                                                                        AAW94261;
                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                        Query Match
                                                                       Tang YT
Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOLT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRAV/)
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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural clement (TTSE) which is covalently linked to at least one heterologous moiety, the TTSE baing capable of forming a stable complex with 2 other moiety, the TTSE baing capable of forming a stable complex with 2 other any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN12 GAM94261 to AAM94261 to AAM94264). The TTSE can be used for the construction of conjugates with heterologous moietys and such as a radioactive moiety, a cytokine, a non-proteinaceous polymer, a photo cross-linking agent, or a group facilitating conjugation of the monomer polypeptide construct to a target. They can be used as vehicles for sesembling antibody fragments into oligomeric or multivalent constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific population of cells. They can also be used for delivering a substance to a city of the support of an entity of the material for transfection or infection of the specific a cell or tissue or for delivering an imaging or transferd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibody to a tumour. They can also be used for prevention or treating a disease or for diagnosis. The TTSE provides a stable structure which can act as a vehicle for a wide variety of conjugates. The present sequence represents a CIHEFXTAN123 fusion protein sequence. The specification claims that the heterologous molety to which the TTSEs of the invention are linked to is specifically different from the present fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
New monomer polypeptide constructs for diagnosis and therapy - comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasminogen activation; clot lysis; fibrinolysis; tissue growth; tissue repair; haemostasis; neoplasia therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of chain of Tetranectin protein.
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                                                                                                                                                                                                               Disclosure; Fig 6; 110pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP60098 standard; protein; 182 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 36; Conservative
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Best Local Similarity
Matches 35; Conserv
                            Example 1; Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW94270;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin.
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                Tetranectin is comprised of four polypeptide chains having the formula shown in AAP60098. Tetranectin stimulates and controls the plasminogen activation resulting in a higher rate of clot lysis or fibrinolysis, esp. in the presence of blood platelets and in the presence of a complex fibrin clot from blood. It stimulates and controls the plasminogen activation in the absence of fibrin but in the presence of a cofactor such as polylysine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New monomer polypeptide constructs for diagnosis and therapy comprise a tetranectin trimerising structural element covalently
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                                                                                                       New Tetranectin protein - purified from human blood plasma by e.g. affinity chromatography on a column with coupled kringle of plasminogen
                                                                                                                                                                                                                                                                  Length 182;
                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kastrup JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Tetranectin polypeptide fragment (residues 1-52).
                                                                                                                                                                                                                                                                  97.1%; Score 167; DB 7;
97.2%; Pred. No. 3.1e-13;
ive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                          1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                     17 VVNTKMFEELKSRLDTLAQEXALLKEQQALQTVCLK 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thogersen HC;
                                                                                                                                                                                                                                                                                                                                                                              AAW94254 standard; Protein; 52 AA.
                                                                                                                                              Claim 9; Page la; 12pp; English.
         86EP-0201005.
                           85NL-0001682.
                                                                  Duhl Clemmensen I, Kluft C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-DK00245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97DK-0000685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Graversen NJH,
                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                               (NEDE ) NEDERLAND ORG TNO.
                                                                                                                                                                                                                                                                                      35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ETZE/) ETZERODT M.
(GRAV/) GRAVERSEN N J H.
(HOLT/) HOLTET T L.
(KAST/) KASTRUP J S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nielsen BB,
                                                                                    WPI; 1986-340760/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-080897/07
                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                               182 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9856906-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
        10-JUN-1986;
                           11-JUN-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Larsen IK,
                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                   Query Match
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antibody to a tumour. They can also be used for prevention or treating a disease or for diagnosis. The TTSE provides a stable structure which can act as a vehicle for a wide variety of conjugates. The present sequence represents a human tetranectin polypeptide fragment. The encoding nucleic acid sequence was amplified by PCR from the plasmid clone pT7H6FXTN123. This is used in the construction of E. coli expression vectors for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                counsider comprises at teast one termineration. Controlled to Comprise at teast one between the controlled to the TTSE, which is covalently linked to at least one heterologous moiety, the TTSE being capable of forming a stable complex with 2 other TTSEs, with the proviso that the heterologous moiety is different from any of the fusion proteins CIH6FXTN123, H6FXTN123, H7FXTN123, H7FX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preselected pharmacokinetic and/or pharmadynamic properties. The constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific population of cells. They can also be used for delivering a substance to a cell or tissue or for delivering an imaging or toxin-conjugated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumur; human; tetranectin.
                                                                                                                                                                                                                                                                                                                      The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
linked to at least one heterologous moiety for providing functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     construct comprise at least one tetranectin trimerising structura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Pred. No. 3.4e-13;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
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                                                                                                                                                                                                 English.
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97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-DK00245.
                                                                                                                                                                                                 59; 110pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ETZE/) ETZERODT M. (GRAV/) GRAVERSEN N J H.
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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein caniform. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural molety, the TYEE being capable of forming a stable complex with 2 other molety, the TYEE being capable of forming a stable complex with 2 other any of the fusion proteins CIH6FWAIN123, H6FWAIN12, H6FWAIN13, H
                                                                                                                                                                                                                                    New monomer polypeptide constructs for diagnosis and therapy - Comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
                                                                                                       Kastrup JS;
                                                                                        Graversen NJH, Holtet TL,
                                                                                                                            Thogersen HC;
                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 4; 110pp; English.
                                                                                                                      Nielsen BB,
   (HOLT/) HOLTET T L. (KAST/) KASTRUP J S.
                                                                                                                                                                             WPI; 1999-080897/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 AA;
                                                                                           Etzerodt M,
                                                                                                                      Larsen IK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sednence
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New monomer polypeptide constructs for diagnosis and therapy - comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional

Example 1; Page 59-60; 110pp; English.

activity

Holtet TL, Kastrup JS;

Graversen NJH, Holter TL,

Nielsen BB,

WPI; 1999-080897/07.

GRAVERSEN N J H. HOLTET T L.

HOLT/)

(ETZE/) ETZERODT M.

(KAST/) KASTRUP J S

Etzerodt M, Larsen IK,

98WO-DK00245 97DK-0000685

11-JUN-1998; 11-JUN-1997;

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Matches
                                                                                                                                                                                                                                                                                                                                                               RESULT 11
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                                                   ö
                                                                                                                                                                                                                                                                                                                                                               Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin.
                                                   Gaps
                                                   ;
0
          Length 73;
                                            1; Indels
                                                                                                                                                                                                                                                                                                                        Tetranectin polypeptide fragment (residues 1-49).
    94.2%; Score 162; DB 20;
97.2%; Pred. No. 4.9e-13;
                                                                         1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
                                                                                               0; Mismatches
                                                                                                                                                                                                            AAW94255 standard; Protein; 49
                                                                                                                                                                                                                                                                                     26-APR-1999 (first entry)
                                        Conservative
                  Local Similarity
les 35; Conserv
Query Match
                                                                                                                                                                                                                                                  AAW94255;
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AAW94255

g ð

Matches

Homo sapiens WO9856906-A1

17-DEC-1998.

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The inventoring retained to the design of trimeric polypeptides using family. The trimeric polypeptide sconstructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural comprise at least one tetranectin trimerising structural comprise at least one tetranectin trimerising structural comprise, which is covalently linked to at least one heterologous and the proviso that the heterologous molety is different from carry of the fusion proteins CIHGEYTN123, HGEYTN123, HG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       act as a vehicle for a wide variety of conjugates. The present sequence represents a human tetranectin polypeptide fragment. The encoding nuclei acid sequence was amplified by PCR from the plasmid clone pT7H6FXTM123. This is used in the construction of E. coli expression vectors for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trimeric polypeptide; tetranectin trimerising structural element; TTSE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the design of trimeric polypeptides using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 154; DB 20; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               production of trimerised chimeric fusion proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.08; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTV 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTV 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW94263 standard; protein; 65 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H6FXTN12 fusion protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Trimeric polypeptide; tetranectin trimerising structural element; 'flusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin.

Homo sapiens. WO9856906-A1

Synthetic

H6FXtripb fusion protein sequence.

26-APR-1999 (first entry)

AAW94271;

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AAW94271 standard; protein; 69 AA.

AAW94271

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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural elements at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous moiety, the TTSE being capable of forming a stable complex with 2 other TTSEs, with the proviso that the heterologous moiety is different from any of the fusion proteins CIHGEYTN123, HEYTN123, HEYTN13, HEYTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibody to a tumour. They can also be used for prevention of treating a disease or for diagnosis. The TYSE provides a stable structure which can act as a vehicle for a wide variety of conjugates. The present sequence represents a H6FXTN12 fusion protein sequence. The specification claims that the heterologous moiety to which the TYSEs of the invention are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 that the heterologous moiety to which the TTSEs of the invention are inked to is specifically different from the present fusion protein
fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; H6FXTN12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New monomer polypeptide constructs for diagnosis and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kastrup JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IH, Holtet TL,
Thogersen HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 8; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-DK00245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97DK-0000685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NJH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Graversen N
Nielsen BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETZERODT M.
GRAVERSEN N J H.
HOLTET T L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KAST/) KASTRUP J S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-080897/07
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                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                        WO9856906-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Etzerodt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Larsen IK,
                                                                                                                                                                                              Synhtetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ETZE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HOLT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GRAV/)
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comprise a tetranectin trimerising structural element covalently linked to at least one heterologous molety for providing functional

Disclosure; Fig 4; 110pp; English.

activity

New monomer polypeptide constructs for diagnosis and therapy

Kastrup JS;

JH, Holtet TL, Thogersen HC;

Graversen NJH,

Etzerodt M, Larsen IK,

Nielsen BB,

WPI; 1999-080897/07.

GRAVERSEN N J H.

(HOLT/) HOLTET T L. (KAST/) KASTRUP J S. (ETZE/) ETZERODT M. (GRAV/) GRAVERSEN N

98WO-DK00245. 97DK-0000685

.1-JUN-1998; 11-JUN-1997;

17-DEC-1998.

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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous moiety, the TTSE being capable of forming a stable complex with 2 other TTSE being capable of forming a stable complex with 2 other TTSEs, with the proviso that the heterologous moiety is different from any of the fusion proteins CIHEKTWI23, HEKTWI23, HEKTWI23 (AAW94261 to AAW94264). The TTSE can be used for the construction of conjugates with heterologous moieties such as a ligand binding structure, a toxin, a detectable label, an in situ activatable substance, an enzyme, a radioactive mobiety, a cytckine, a non-proteinaceous polymer, a photo cross-linking agent, or a group facilitating conjugation of the monem polypeptide construct to a target. They can be used as vehicles for assembling antibody fragments into oligomeric or multivalent centities for generating chimeric artificial antibodies having a protein and for target the therapy involving solorities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody to a tumour. They can also be used for prevention or treating a disease or for diagnosis. The TYSE provides a stable structure which can act as a vehicle for a wide variety of conjugates. The present sequence represents a H6FXtripb fusion protein sequence encoded by the plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    population of cells. They can also be used for delivering a substance to a cell or tissue or for delivering an imaging or toxin-conjugated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 AA;
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0;

Gaps

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Length 65; Indels

DB 20; 4.3e-12; thes 0;

89.5%; Score 154; DB 100.0%; Pred. No. 4.3e ive 0; Mismatches

1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTV 33

33; Conservative

Query Match Best Local Similarity Matches 33; Conserv

33

g

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Length 69;

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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural construct comprise at least one tetranectin trimerising structural moiety, the TTSE being capable of forming a stable complex with 2 other any of the fusion proteins CIHERYANI3, HERYANI3, HERYANI2, HERYANI2, CAMA94261 to AAM94264). The TTSE can be used for the construction of conjugates with heterologous moieties such as a ligand binding conjugates with heterologous moieties such as a ligand binding at a radioactive moiety, a cytokine, a non-proteinaceous polymer, a photo cross-linking agent, or a group facilitating conjugation of the monomer polypeptide construct to a target. They can be used as vehicles for assembling antibody fragments into oligomeric or multivalent mannity and an entity and entity and entity and an entity and an entity and an entity and entit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preselected pharmacokinetic and/or pharmadynamic properties. The constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific population of cells. They can also be used for delivering a substance to a cell or tissue or for delivering an imaging or toxin-conjugated antibody to a tumour. They can also be used for prevention or treating a disease or for diagnosis. The TTSE provides a stable structure which can
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New monomer polypeptide constructs for diagnosis and therapy - comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trimeric polypeptide; tetranectin trimerising structural element; 1 fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; ubiquitin.
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                       Indels
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0
         0; Mismatches
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                                                                                1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQT
                                                                                                                                   36 VVNTKMFEELKSRLDTLAQEVALLKEQQALQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Graversen NJH, Holtet TL
Nielsen BB, Thogersen HC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H6FXtripB-UB fusion protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                  AAW94266 standard; protein; 145 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Fig 14; 110pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97DK-0000685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
    Conservative
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GRAVERSEN N J H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nielsen BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HOLT/) HOLTET T L. (KAST/) KASTRUP J S.
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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural construct comprise at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous constructs, the TTSE being capable of forming a stable complex with 2 other TTSEs, with the provise that the heterologous moiety is different from any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN123, GAN94261 to AAN94264). The TTSE can be used for the construction of conjugates with heterologous moieties such as a ligand binding structure, a texin, a detectable label, an in situ activatable substance, an enaryme, a radioactive moiety, a cytokine, a non-proteinaceous polymer, a photo cross-linking agent, or a group facilitating conjugation of the monomer polypeptide construct to a target. They can be used as vehicles for assembling antibody fragments into eligomeric or multivalent
act as a vehicle for a wide variety of conjugates. The present sequence represents a H6FXLripB-UB (ubiquitin) fusion protein sequence encoded by the plasmid pH6FXLripB-UB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein; ligand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tumour; human; tetranectin; CEA6.
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New monomer polypeptide constructs for diagnosis and therapy - comprise a tetranectin trimerising structural element covalently linked to at least one heterologous moiety for providing functional
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                                                                                                                Score 150; DB 20;
Pred. No. 3.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                  H6FXscFv(CEA6)tripB fusion protein sequence.
                                                                                                                    87.4°,
100.0%; Pred. nc.
''.a 0; Mismatches
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Thogersen HC;
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                                                                                                                                                     Conservative
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(GRAV/) GRAVERSEN N J H.
(HOLT/) HOLTET T L.
(KAST/) KASTRUP J S.
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Larsen IK, Nielsen BB,
                                                                                                                                  Best Local Similarity
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preselected pharmacokinetic and/or pharmadynamic properties. The constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific population of cells. They can also be used for delivering a substance to an tibody to a tumour. They can also be used for prevention or treating a cell or tissue or for delivering an imaging or toxin-conjugated antibody to a tumour. They can also be used for prevention or treating a disease or for diagnosis. The TTSE provides a stable structure which can act as a vehicle for a wide variety of conjugates. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        Trimeric polypeptide; tetranectin trimerising structural element; TTSE; fusion protein: ilgand binding structure; toxin; enzyme; cytokine; artificial antibody; pharmacokinetic; pharmadynamic; gene therapy; transfection; imaging; tunur; human; tetranectin; CRA6.
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Thogersen HC;
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nes 32; Conserv
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The invention relates to the design of trimeric polypeptides using polypeptide structural elements derived from the tetranectin protein family. The trimeric polypeptides constructed as a monomer polypeptide construct comprise at least one tetranectin trimerising structural element (TTSE) which is covalently linked to at least one heterologous moiety, the TTSE being capable of forming a stable complex with 2 other TTSEs, with the proviso that the heterologous moiety is different from

linked to at least one heterologous moiety for providing functional New monomer polypeptide constructs for diagnosis and therapy comprise a tetranectin trimerising structural element covalently

WPI; 1999-080897/07.

Example 4; Fig 18; 110pp; English.

activity

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any of the fusion proteins CIIH6FXTN123, H6FXTN123, H6FXTN12, H6FXTN12

(AAM94261 to AAM94264). The TTSE can be used for the construction of conjugates with heterologous moleties such as a ligand binding such as a ligand binding and binding activated label, an in stu activatable substance, an enzyme, a radioactive moiety, a cytokine, a non-proteinaceous polymer, a photo cross-linking agent, or a group facilitating conjugation of the monomer polypeptide construct to a target. They can be used as vehicles for assembling antibody fragments into oligomeric or multivalent entities for generating chimeric artificial antibodies having preselected pharmacokinetic and/or pharmadynamic properties. The constructs can be used for targeted gene therapy involving selective delivery of the material for transfection or infection of the specific conjutation of cells. They can also be used for delivering a substance to a cell or tissue or for delivering an imaging or toxin-conjugated antibody to a tumour. They can also be used for prevention or treating a cell or tissue or for delivering an imaging or toxin-conjugated antibody to a tumour. They can also be used for prevention or treating a classes or for diagnosis. The TTSE provides a stable structure which can a task as a weblice for a wide variately of conjugates. The presents a HERYLINGENOUS.
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100.0%; Pred. No. 8e-11;
ive 0; Mismatches 0; Indels
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Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thoegersen, Hans Christian
APPLICANT: Holtet, Thor Las
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: Improved method for the refolding
TITLE OF INVENTION: proteins
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 172; DB 1;
Pred. No. 3.5e-16;
             CONNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,486
FILING DATE:
                                                                                                                                                                                                        US-08-247-491A-5
US-08-129-456A-36
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US-09-123-615-3
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PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 56, Application US/08469486 Patent No. 5739281 GENERAL INFORMATION:
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Best Local Similarity
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CITY: Boston
STATE: Massach
COUNTRY: USA
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105.923 Million cell updates/sec
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                                                                                                      April 15, 2003, 11:45:59; Search time 10 Seconds
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
              GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
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-08-469-658-56
-09-602-877A-99
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US-08-669-408B-10
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq
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Score

Result Ş Gaps

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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER FILE REFERENCE: 210121.446CS
CURRENT APPLICATION NUMBER: US/09/602,877A
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 107
SOFTHARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                      43.6%; Score 75; DB 4; Length 197; 57.1%; Pred. No. 0.0059; ive 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Reld, Robert A.
APPLICANT: Reld, Robert A.
APPLICANT: Hemperly, Dohn J.
TITLE OF INVENTION: HUMAN RESTRICTIN AND NUCLEIC ACID
NUMBER OF SEQUENCES.
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,665
                                                                                                                                                                                                                                                                                                                                                                                                                                   9 ELKSRLDTLAQEVALLKEQQALQTVCLK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :||:::: | || || || |||||||||: 43 DLKTQIEKLWTEVNALKEIQALQTVCLR 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08404665
Patent No. 5591583
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: FUGIL, Donna R.
REGISTRATION NUMBER: 32,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1358 amino acids
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.11
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1 Becton Drive
CITY: Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Company
                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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COUNTRY: U
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                                                                                                                                                                                                                                                                                   US-09-602-877A-99
                                                                                                                                                                                 SEQ ID NO 99
LENGTH: 197
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               Gaps
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0
                                                                                                                                                                                                             Sequence 56, Application US/08469658
Fatent No. 5917018
GENERAL INFORMATION:
APPLICANT: The gersen, Hans Christian
APPLICANT: Holtet, Thor Las
APPLICANT: BL2erodt, Michael
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSES: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 202;
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100.0%; Pred. No. 3.5e-16;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIALDE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: Pat.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,658
FILING DATE: February 4, 1994
CLASSIFICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
CLASSIFICATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 30,162
RECISTRATION NUMBER: 30,162
                                              1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
                                                                          38 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 73
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  Conservative
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Best Local Similarity 100.
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 202 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-469-658-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02110-2804
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                                                                                                                                                                                         US-08-469-658-56
36;
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Matches
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Ouery Match

Query Match

Query Match

Query Match

Query Match

Best Local Similarity 36.0%; Pred. No. 80;

Matches 9; Conservative 11; Mismatches 5; Indels 0; Gaps 0

Qy 3 NTKMFEELKSRLDTLAQEVALLKEQ 27

Qy 3 NTKMFEELKSRLDTLAQEVALLKEQ 27

Db 130 SAQVLQELLSRIEMLEREVSVLRDQ 154

RESULT 3 US-09-602-877A-99 Sequence 99, Application US/09602877A Facent No. 6432707

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.

RESULT 5

Gaps

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APPLICANT: Reed, Steven G.
APPLICANT: Campos Neto, Antonio
APPLICANT: Campos Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                    Length 1358;
                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                    ; Score 52; DB
; Pred. No. 80;
11; Mismatches
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                                 FILLNE DALE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION UNMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3341
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1358 amino acids
        APPLICATION NUMBER: US/08/404,781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 41, Application US/09183861
; Patent No. 6365165
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/022,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILLING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVID 3.
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21017
TELEPHONE: (200) 622-4900
TELEPHONE: (200) 622-4901
INFORMATION FOR SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Leishmania major
                                                                                                                                                                                                                                                                                                                                    30.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserval
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 C
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                              US-08-404-781-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
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80;
                                                             APPLICANT: Reid, Robert A.
APPLICANT: Ackley, Rhonda L.
APPLICANT: Hemperly, John J.
TITLE OF INVENTION: BEQUENCES
TITLE OF INVENTION: SEQUENCES
TORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
ADDRESSEE: Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-404-781-4
Sequence 4, Application US/08404781
Patent No. 5681931
GENERAL INFORMATION:
APPLICANT: Reid, Robert A.
APPLICANT: Ackley, Rhonda L.
APPLICANT: Hemperly, John J.
TITLE OF INVENTION: HUMAN RESTRICTIN AND NUCLEIC ACFD: TITLE OF INVENTION: SEQUENCES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
ADDRESSEE: Company
                                                                                                                                                                                                                                                                                                                            ZIP: 07417
ZIP: 07417
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
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130 SAQVLQELLSRIEMLEREVSVLRDQ 154
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Sequence 4, Application US/08404671
Patent No. 5635360
GENERAL INFORMATION:
APPLICANT: Reid, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATORNEX/AGENT INFORMATION:
NAME: FUGIL, Donna R.
REGISTRATION NUMBER: 32,135
REFRENCE/POCKET NUMBER: P-33.
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1358 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
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CITY: Franklin Lakes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
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HUANG, WEIDONG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-882-238A-1
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Petent No. 6375955
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Webb, John R.
APPLICANT: Webb, John R.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHWANIA ANTIGENS FOR USEIN THE THERAPY AND NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
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                                     Score 50; DB 4; Length 169;
Pred. No. 13;
3; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: WEAL

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/022,765

FILING DATE: 12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                       SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210121.420C3
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APPLICANT: NGUYEN, THAI D.
APPLICANT: POLANSKY, JON R.
                                                                                                                              |||: |||| |: | |: | |
|144 EELQORLDTATQQRAELEAQVA 165
                                                                                                       8 EELKSRLDTLAQEVALLKEQQA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 231
REFERENCE/POCKET NUMBER: 211
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||||: |||| |: | |: | |
144 EELQORLDTATQORAELEAQVA 165
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                                   29.1%;
54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                 Query Match
Best Local Similarity 54.5
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 12; Conserva
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TELEFAX: (;
                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
US-09-183-861-41
                                                                                                                                                                                                             US-09-022-765-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-645-900A-1
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Gaps
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                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,900A
FILING DATE: 14 MAY 1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MARE: MARE: DAVID
REGISTRATION NUMBER: 41,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEPHONE: (202) 383-7451
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS OF TITLE OF INVENTION: GLAUCOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NGOYEN, THAI D.
APPLICANT: POLANSKY, JON R.
APPLICANT: HORNEKY, JON R.
APPLICANT: HORNEKY, JON R.
APPLICANT: HORNEY, WEIDONG
TITLE OF INVENTION: GLAUCOMA
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50; DB 2;
Pred. No. 46;
4; Mismatches
                                             STREET: 1299 PENNSYLVANIA AVE., N.W. CITY: WASHINGTON STATE: D.C. COUNTRY: US ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.1%; Score 50; 48.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: HOWREY & SIMON
1299 PENNSYLVANIA AVE., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/882,238A
FILING DATE: 25 JUNE 1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5854415
                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           504 amino acids
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NAME: MARSH, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 29.1
Best Local Similarity 48.0
Matches 12; Conservative
                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & 9
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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GENERAL INFORMATION:
APPLICANT: NGUYEN, Thai D.
APPLICANT: POLANSKY, JON R.
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND
TITLE OF INVENTION: RELATED DISEASES
NUMBER OF SEQUENCES: 32
                                                                                                                                                           TITLE OF INVENTION: Methods for the Diagnosis of Glaucoma FILE REFERENCE: 07425.0056
CURRENT APPLICATION UNBER: US/09/220,459
CURRENT FILING DATE: 1989-12-24
EARLIER FILING DATE: 1999-06-25
EARLIER FILING DATE: 1997-06-25
EARLIER FILING DATE: 1996-05-17
EARLIER FILING DATE: 1996-05-17
EARLIER FILING DATE: 1996-05-17
EARLIER FILING DATE: 1996-10-20
EARLIER FILING DATE: 1999-11-03
EARLIER FILING DATE: 1994-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.1%; Score 50; DB 4;
48.0%; Pred. No. 46;
tive 4; Mismatches 9
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SOFWARE: FSSLSEO for Windows Version 2.0
CNERRWI APPLICATION DATA:
APPLICATION NUMBER: US/08/938,669A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Howrey & Simon
1299 Pennsylvania Avenue, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P-42,878
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-6857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 32, Application US/08938669A Patent No. 6171788
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APPLICATION NUMBER: 08/791,154
FILING DATE: 28-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                         Sequence 1, Application US/09220459 Patent No. 6150161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Mendelson, Elliot
REGISTRATION NUMBER: P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 29.19
Best Local Similarity 48.09
Matches 12; Conservative
                                                                                 GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D
APPLICANT: Polansky, Jon R
APPLICANT: Huang, Weidong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 3 SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1222
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ZIP: 20004-2402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-938-669A-32
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LENGIH: 504
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48.0%; Pred. No. 46;
tive 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                               Length 504
                                                                                                                                                                                                                                                                                                         9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: NGUYEN, THAI D.
APPLICANT: POLANSKY, JON R.
APPLICANT: HUANG, WEIDONG
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS OF
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS OF
TITLE OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: HOWREY & SIMON
STREET: 1299 PERNNYLVANIA AVE., N.W.
CITY: WASHINGTON
STREET: D.C.
COUNTRY: US
21P: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/667,790A
FILING DATE: 21 JUNE 1996
CLASSIFICATION:
                                                                                                                                                                                                                                                               29.1%; Score 50; DB 2; 48.0%; Pred. No. 46;
                                                                                                                                                                                                                                                                                                         4; Mismatches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08667790A
Patent No. 5861497
                                       TELEFAX: (202) 383-7451
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: amino acid
STARNEDNESS: single
REGISTRATION NUMBER: 41,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MARSH, DAVID
REGISTRATION NUMBER: 41,408
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: No. 5854415e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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US-08-667-790A-1
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                                                                                                                                                                                                                                                                                  Best Local Similarity 48.09
Matches 12; Conservative
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Matches 12; Conserv
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                                   TELEPHONE:
TELEFAX: (
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                                                                                                                                                                                                                       US-08-882-238A-1
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Length 504 Indels

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US-09-056-285A-8
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Patent No. 6548867
GENERAL INFORMATION:
APPLICANT: NGIVEN, THAI D.
APPLICANT: NGIVEN, THAI D.
APPLICANT: HUNGY, MEIDONG
TITLE OF INVENTION: GLAUCOMA
NUMBER OF SEQUENCES: 3
CORRESPONDENCES: 3
CORRESPONDENCES: ADDRESSEE: HOWERY & SINON
STREET: 1299 PENNSYLVANIA AVE., N.W.
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk Compatible COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/546,568B FILING DATE: 20 October 1995 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION: NAME: MARSH, DAVID RESISTRATION UNMBER: 41,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                        29.1%; Score 50; DB 48.0%; Pred. No. 46; tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.1%; Score 50; DB 48.0%; Pred. No. 46; tive 4; Mismatches
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164 ENLARRLESSSQEVARLRRGQCPQT 188
                                                                                                                                                                                                                                                                                               8 EELKSRLDTLAQEVALLKEQQALQT 32
                             INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS: LENGTH: 504 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: Linear MOLECULE TYPE: protein FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: No. 6248867e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 504 amino acids TYPE: amino acid
                                                                                                                                                                                                                                      Best Local Similarity 48.0 Matches 12; Conservative
TELEFAX: 202 383-6610 TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 48.0%
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C.
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                 US-08-938-669A-32
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Gaps
Sequence 8, Application US/09056285A
Patent No. 6403307
GENERAL INFORMATION:
GENERAL INFORMATION:
Sheffield, Val C.
Alward, Wallace L.M.
Fingert, John
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 29.1%; Score 50; DB 4; Length 504; Best Local Similarity 48.0%; Pred. No. 46; Matches 12; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
COMPUTER: TEADABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,285A
FILING DATE: 07-APT-1998
ATTORNEY_AGGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REGISTRATION NUMBER: 35,430
RELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                  ADDRESSEE: FOLEY, HOAG & ELLOT LLP
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-056-285A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: April 15, 2003, 11:51:48
Job time : 12 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 EELKSRLDTLAQEVALLKEQQALQT 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 504 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                     STATE: MA
                                                                                                                                                                                                                                                                                                                               COUNTRY:
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Gaps

; 0

9; Indels

8 EELKSRLDTLAQEVALLKEQQALQT 32

QΩ ò

RESULT 15

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GenCore version 5.1.4_p5_4578

Copyright (c) 1993 - 2003 Compugen Ltd:

OM protein - protein search, using sw model

Run on: April 15, 2003, 11:50:25; search time 10 Seconds

(without alignments)
220.090 Million cell updates/sec

Perfect score: 172
Sequence: 172
Sequence: 1 VVNTKMFEELKSRLDTLAQEVALLKEQOALQTVCLK 36
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 248812 seqs, 61136040 residues

Total number of hits satisfying chosen parameters: 248812

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

Published_Applications_AA:*

Database

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
	172	100.0	36	- 6	115-09-987-107-39	fact 95 acreames
2	172	100.0		0	115-09-924-340-62	, ,
ım	172	100.0	202	0	US-09-992-600A-62	
4	167	97.1		0	US-09-987-107-12	
S	162	94.2	58	6	US-09-987-107-13	3
9	162	94.2	258	6	US-09-987-107-4	4 . A
7	162	94.2	273	σ	US-09-987-107-50	50
80	162	94.2	301	σ	US-09-987-107-3	3.
6	162	94.2	301	6	US-09-987-107-5	
10	162	94.2	304	6	US-09-987-107-6	Sequence 6, Appli
11	162	94.2	304	σ	US-09-987-107-7	7
12	162	94.2	304	6	US-09-987-107-8	8
13	162	94.2	306	6	US-09-987-107-9	Sequence 9, Appli
14	162	94.2	306	σ	US-09-987-107-10	10,
15	162	94.2	306	6	US-09-987-107-11	11,
16	162	94.2	316	σ	US-09-987-107-48	48,
17	162	94.2	316	σ	US-09-987-107-54	54,
18	162	94.2	323	6	US-09-987-107-56	56,
19	162	94.2	323	6	US-09-987-107-58	58,

Sequence 60, Appl Sequence 64, Appl Sequence 66, Appl Sequence 40, Appl Sequence 41, Appl Sequence 91, Appl Sequence 91, Appl Sequence 10, Appl Sequence 403, Appl Sequence 276, Appl		Length 36; Indels 0; Gaps 0; ES THEREOF
US-09-987-107-60 US-09-987-107-62 US-09-987-107-64 US-09-987-107-46 US-09-987-107-40 US-09-987-107-41 US-09-745-288-99 US-09-938-418-10 US-09-938-418-10 US-09-932-598-403 US-09-992-598-403 US-09-999-735-403 US-09-999-730-403 US-09-999-730-403 US-09-991-687-403	ALIGNMENTS 9987107 PROTEINS ANALOGUES US/09/987,107 11-13 5 60/264,022 5 60/264,022 6 PA2001 00057 7 PA2000 01682 10	100.0%; Score 172; DB 9; Length 36; 100.0%; Pred. No. 3.4e-16; Vative 0; Mismatches 0; Indels LDTLAQEVALLKEQQALQTVCLK 36
994.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.	PULICATION US/(0020156007A1 AVERSEN, JONAS GESTRUP, SOFEN THION: APOLION E: GRAVERSENA (CATION NUMBER: US DATE: 2001-01-1 TION NUMBER: US TIO	
20 21 22 22 23 24 25 25 26 27 26 27 29 30 31 31 31 32 33 34 45 40 40 41 42 43 43 44 43 43 44 43 45 45 46 47 47 48 48 48 48 48 48 48 48 48 48 48 48 48	RESULT 1 US-09-987-107-39 Sequence 39, A Fatent No. US2 GENERAL INFORM APPLICANT: GR APPLICANT: M TITLE OF INVE FILE REPRENC CURRENT FILING PRIOR APPLICAN PRIOR FILING NUMBER OF SEQ SOFTWARE: PAL SOFTWARE: PAL SOFTWARE: PAL SOFTWARE: PAL CHARLES PAL SOFTWARE: PAL	Query Match Best Local Similarity Matches 36; Conser Oy 1 VVNTKMFEELKSR Oy 1 VVNTKMFEELKSR Db 1 VVNTKMFEELKSR RESULT 2 US-09-924-340-62 Sequence 62, Applicat Publication No. US200 GENERAL INFORMATION: APPLICANT: Bejanin, APPLICANT: Tanaka, TITLE OF INVENTION:
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Length 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.3e-15;
hes 0;
                                                                                                                                                                           APPLICANT: MOESTRUP, Soren
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REPERBENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-01-26
PRIOR PLICATION NUMBER: US PA2001 00057
PRIOR PLICATION NUMBER: DK PA2001 00057
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
APPLICANT: MOSSTRUP, Soren
TILE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.1%; Score 167; DB
100.0%; Pred. No. 2.3
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
PRIOR PILING DATE: 2001-01-15
PRIOR PILING DATE: 2001-11-10
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PATENT OF SEQ ID NOS: 91
SOFTWARE: PATENT VERSION 3.1
SEQ ID NO: 13
LENGTH: 58
                                                                                        Sequence 12, Application US/09987107
Patent No. US20020156007A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)...(4)
TOTHER INFORMATION: Linker sequence
NAME/KEY: misc_feature
LOCATION: (5)..(56)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/09987107 Patent No. US20020156007A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Modified TTSE
                                                                                                                                                            APPLICANT: GRAVERSEN, Jonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 97.1
Best Local Similarity 100.
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 94.2
Best Local Similarity 97.2
Matches 35; Conservative
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OTHER INFORMATION: Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (1)..(4)
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LOCATION: (57)..(58)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                        GENERAL INFORMATION:
                                                               US-09-987-107-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: HOR
US-09-987-107-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 12
LENGIH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JERERAL INFORMATION:
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TILE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.054.01V
CURRENT FILING DATE: 2001-11-13
PRIOR PLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-07-13
PRIOR PLICATION NUMBER: US 60/302,277
PRIOR PLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR PLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-06-15
SOFTWARE: JPatent
SOFTWARE: JPatent
SEQ ID NO 62
LENGTH: 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 202;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 172; DB 9;
100.0%; Pred. No. 2.6e-15;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 172; DB 9;
100.0%; Pred. No. 2.6e-15;
ive 0; Mismatches 0;
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CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
SOFTWARE: JPALENT DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-992-600A-62

, Sequence 62, Application US/09992600A

; Publication No. US20030027161A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 36; Conservative
FILE REFERENCE: 91.US2.REG
CURRENT APPLICATION NUMBER
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                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 36; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: SIGNAL
; LOCATION: 1. 21
US-09-924-340-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: SIGNAL
; LOCATION: 1. 21
US-09-992-600A-62
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Gaps

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Length 273;
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                                                                          Indels
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OTHER INFORMATION: Trimerisation module from tetranectin NAME/FET: misc_deature
LOCATION: (59)..(301)
OTHER INFORMATION: Mature ApoAl
Score 162; DB 9; I
Pred. No. 7.7e-14;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRNERAL INFORMATION:
APPLICANT: GRAVERSEN, JONAS
APPLICANT: MOESTRUP, SCOREN
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILLING DATE: 2001-11-13
PRIOR FILLING DATE: 2001-11-13
PRIOR FILLING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: DK PA2001 00057
PRIOR FILLING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR FILING DATE: 2001-11-13
SOFTWARR: PALENTIN OF SEQ ID NOS: 91
SOFTWARR: PALENTIN VEFSION 3.1
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APPLICANT: GRAVERSEN, Jonas
APPLICANT: GRAVERSEN, JONAS
APPLICANT: MOESTRUP, SCOREN
TITLE OF INVENTION: APPLICAPINS: APPLICATION OF APP
                                                                                                                                             1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
                                                                                                                                                                                      36 VVNTKMFEELKSRLDTLAQEVALLKEQOALQTVSLK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
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                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                         US-09-987-107-3
; Sequence 3, Application US/09987107
; Patent No. US20020156007A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-09-987-107-5
; Sequence 5, Application US/09987107
; Patent No. US20020156007A1
   94.28;
97.28;
                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
   Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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US-09-987-107-50
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LOCATION: (1)..(58)
OTHER INFORMATION: Trimerisation module from tetranectin
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LOCATION: (59)..(258)
CTHEN INFORMATION: Amion acids 68-267 from human Apo Al
US-09-987-107-4
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94.2%; Score 162; DB 9;
Best Local Similarity 97.2%; Pred. No. 7.2e-14;
Matches 35; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                         SERENT INFORMATION:
APPLICANT: GRAVERSEN, Jonas
APPLICANT: GRAVERSEN, Jonas
APPLICANT: MESTRUP, SCREEN
TITLE OF INVENTION: APOLITOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
CURRENT FILING DATE: 2001-11.13
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
SPRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
SSC ID NO 4-4
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TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2001 00057
PRIOR FILING DATE: 2001-01-15
PRIOR PILING DATE: 2001-01-15
PRIOR PILING DATE: 2000-01-15
SOFTWARE: PALENTING NUMBER: DK PA2000 01682
LENGTH: 273
                                     21 VVNTKMFEELKSRLDTLAQEVALLKEQOALQTVSLK 56
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1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
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Patent No. US2002215607A1
GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
                                                                                                                                                                                                                                                 Sequence 4, Application US/09987107
Patent No. US20020156007A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-987-107-50
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Gaps
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LOCATION: (13)...(13)
OTHER INFORMATION: Mutagen
NAME/KEY: misc_feature
LOCATION: (19)...(19)
OTHER INFORMATION: Mutagen
                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 8.7e-14;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                 NAME/KEY: misc_feature
LOCATION: (1)..(58)
UOTHER INFORMATION: Trimerisation module from tetranectin
NAME/KEY: misc_feature
LOCATION: (9)..(9)
OTHER INFORMATION: Mutagen
NAME/KEY: misc_feature
LOCATION: (15)..(15)
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OTHER INFORMATION: Trimerisation module from tetranectin NAME/KEY: misc_feature
LOCATION: (59)..(61)
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Pred. No. 8.6e-14;
0; Mismatches 1
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APPLICANT: MOESTRUP, Soren
TITLE OF INVENTION: APPLIPOPROTEINS ANALOGUES
FILE PEFERENCE: GRAVERSENIA BOSTILIO
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT APPLICATION NUMBER: US 60/264,022
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PATENTIN NUMBER: DK PAZOOO 01682
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 6
LENGTH: 304
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NAME/KEY: misc_feature
LOCATION: (59)..(301)
OTHER INFORMATION: Apo-Al mature
US-09-987-107-5
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Patent No. US20020156007A1
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US-00-987-107-7
Sequence 7, Application US/09987107
Patent No. US20020156007A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (62)..(304)
; OTHER INFORMATION: Mature Apo Al
US-09-987-107-6
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Best Local Similarity 97.2%;
Matches 35; Conservative (
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Best Local Similarity 97.2%;
Matches 35; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: GARAPRESEN, GOARS

APPLICANT: WGESTRIP, SGEN

TITLE OF INVENTION, FOLDOPOTEINS ANLOGUES

FILE REPEBRACE, GRAVERSEN, GOAS

CURRENT PAINTION, FOLDOPOTEINS ANLOGUES

FILE REPEBRACE, GRAVERSEN, GOAS, 107

CURRENT FILING DATE: 2001-11-13

FROM RAPLICATION NUMBER: US 60/264,022

FROM RAPLICATION NUMBER: US 60/21-10

SOOTHANR: PREDILATION NUMBER: US 60/21-10

SOOTHANR: PREDILATION NUMBER: US 60/21-10

SOOTHANR: PROMATION: Fibronectin based linker

NAME/KRY misc_feature

LOCATION: 107, 107

COMETY WARKER misc_feature

LOCATION: 107, 107

SOOTHANK NUMBER: US 60/21-10

OMETY WARKER misc_feature

LOCATION: 107, 107

SOOTHANK NUMBER: US 60/21-10

OMETY WARKER misc_feature

LOCATION: 107

VANTAMPERIKSELMIALARDVALLARDOALOTYCLK 36

DA 21 WUTKAMPERIKSELDTLARDVALLARDOALOTYCLK 36

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DA 21 WUTKAMPERIKSELDTLARDVALLARDOALOTYCLK 36

SOOTHANK NUMBER: US 60/21-10

SOOTHANK NUMBER: US 60/21-10

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OTHER INFORMATION: Trimerisation module from tetranectin
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OTHER INFORMATION: Trimerisation module from tetranectin NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 162; DB 9;
Pred. No. 8.8e-14;
0; Mismatches 1;
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Pred. No. 8.8e-14;
0; Mismatches 1;
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TITLE OF INVENTION: APPLICANTS
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
PRIOR PLING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
PRIOR PLING DATE: 2001-01-26
PRIOR PLING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2001 00057
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR FILING DATE: 2000-01-15
PRIOR FILING DATE: 2000-11-10
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                                                                                                                                                                                                                                                           OTHER INFORMATION: (63)
OTHER INFORMATION: Tetranectin based linker
LOCATION: /**.
  PRIOR APPLICATION NUMBER: DK PA2000 01682 PRIOR FILING DATE: 2000-11-10 NUMBER OF SEQ ID NOS: 91 SOFTWARE: PatentIn version 3.1 SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09987107
Patent No. US20020156007A1
                                                                                                                                                                                                                                                                                                                                           LOCATION: (64)..(306)
CTHER INFORMATION: Mature Apo Al
US-09-987-107-10
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OTHER INFORMATION: Mature Apo
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NAME/KEY: misc_feature
LOCATION: '10.
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Best Local Similarity 97.29
Matches 35; Conservative
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APPLICANT: GRAVERSEN, Jonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (19)..(19)
OTHER INFORMATION: Mutagen
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Best Local Similarity 97.2
Matches 35; Conservative
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LOCATION: (57)..(63)
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US-09-987-107-11
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LENGTH: 306
                                                                                                                                    TYPE: PRT
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COTHER INFORMATION: Trimerisation module from tetranectin NAME/REY: misc_feature
LOCATION: (59)..(63)
COTHER INFORMATION: Linker
NAME/REY: misc_feature
LOCATION: (54)..(306)
COTHER INFORMATION: Mature Apo Al
US-09-987-107-9
                                                                                                         Score 162; DB 9;
Pred. No. 8.7e-14;
0; Mismatches 1
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94.2%; Score 162; DB 9;
Best Local Similarity 97.2%; Pred. No. 8.8e-14;
Matches 35; Conservative 0; Mismatches
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TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
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APPLICANT: GRAVERSEN, JODAS
PAPLICANT: GRAVERSEN,
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVESENIA
CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT PILING DATE: 2001-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2000-11-10
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: DK PA2001 00057
PRIOR FILING DATE: 2001-01-15
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Patent No. US20020156007A1
                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/09987107
Patent No. US20020156007A1
; NAME/KEY: misc_feature
; LOCATION: (62)..(304)
US-09-987-107-8
                                                                                                       Query Match 94.2%;
Best Local Similarity 97.2%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                     Patent NO. GENERAL INFORMATION:
APPLICANT: GRAVERSEN, JOHAS
APPLICANT: MARSTRUP, SOFEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-987-107-10
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Search completed: April 15, 2003, 12:06:34 Job time: 11 secs

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April 15, 2003, 11:48:05 ; Search time 183 Seconds (without alignments) 126.833 Million cell updates/sec
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1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
11: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
12: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US090_COMB.pep:*
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/cgn2_6/ptodata/1/paa/VG100_COMB.pep:*
/cgn2_6/ptodata/1/paa/VG10_COMB.pep:*
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                         172
1 VVNTKMFEELKSRLDTLAQEVALLKEQOALQTVCLK 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4569144 seqs, 644733110 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                               US-09-445-576A-36
                                                                                                                                                                                                                                                                               Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description		Sequence 35, Appl	Sequence 39, Appl	Sequence 13425, A	Sequence 13425, A	Sequence 27, Appl	Sequence 7, Appli
SUMMARIES			ID	,	US-09-445-576-35	US-09-987-107-39	US-09-834-366-13425	US-60-197-873-13425	US-09-445-576-27	US-09-445-576-7
	d P		DB		18	23	22	27	18	18
			ore Match Length DB II		36	36	95	95	180	181
		Query	Match		100.0	100.0	100.0	100.0	100.0	100.0
			Score		172	172	172	172	172	172
		Result	NO.		1	7	3	4	2	9

Score 172; DB 18; Length 36; Pred. No. 1e-15;

100.0%; 100.0%;

Query Match Best Local Similarity

; TYPE: PRT ; ORGANISM: human US-09-445-576-35

Sequence 41342, A Sequence 62, Appl Sequence 579, Appl Sequence 14, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 14, Appl Sequence 15, Appl Sequence 15, Appl Sequence 16, Appl Sequence 17, Appl Sequence 16, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 11, Appl Sequence 54, Appl Sequence 64, Appl Sequence 26, Appl Sequence 26, Appl Sequence 29, Appl Sequence 20, Appl Sequence 20	
US-09-445-576-25 US-09-791-537-41342 US-09-924-304-62 US-09-934-500-62 US-09-934-500-62 US-09-934-500-62 US-09-934-500-62 US-10-000-489-62 US-09-944-576-62 US-09-445-576-44 US-09-987-107-12 US-09-987-107-13 US-09-987-107-3 US-09-987-107-5 US-09-987-107-5 US-09-987-107-5 US-09-987-107-5 US-09-987-107-5 US-09-987-107-5 US-09-987-107-5 US-09-987-107-5 US-09-987-107-5 US-09-987-107-6 US-09-987-107-5 US-09-987-107-5 US-09-987-107-5 US-09-987-107-6 US-09-987-107-5 US-09-987-107-5 US-09-987-107-5 US-09-987-107-6 US-09-987-107-5 US-09-987-107-6	ALIGNMENTS 1017 1 10245-576-35 Gequence 35, Application US/09445576 FENERAL INFORMATION: APPLICANT: Etzerodt, Michael APPLICANT: Etzerodt, Michael APPLICANT: Graversen, Niels Jonas Heilskov APPLICANT: Graversen, Niels Jonas Heilskov APPLICANT: Graversen, Niels Jonas Heilskov APPLICANT: Malsen, Bettina Bryde APPLICANT: Larsen, Ingrid Kjoller APPLICANT: Larsen, Ingrid Kjoller TITLE OF INVENTION: Trimerising module FILE REFERENCE: THOGERSEN =1 CURRENT APPLICATION NUMBER: US/09/445,576 CURRENT FILING DATE: 1998-06-11 PRIOR FILING DATE: 1998-06-11 PRIOR FILING DATE: 1997-06-11 NUMBER OF SEQ ID NOS: 60 SOFTWARE: PatentIn Ver. 2.0 LENGTH: 36 LENGTH: 36 LENGTH: 36
7.20.20.20.20.20.20.20.20.20.20.20.20.20.	US/094 Ins Chr Chael Las Las Lesa te San tina B Id Kjo O0-07-5 PCT/1 05-11
01000000000000000000000000000000000000	ation I iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii
01010101010101010000000000000000000000	ALI 776-35 35, Application US/09445576 INFORMATION: WIT: ELZEROGL, Michael WIT: ELZEROGL, Michael WIT: HOLtet, Thor Las WIT: Graversen, Niels Jonas H WIT: Kastrup, Jette Sandholm WIT: Kastrup, Jette Sandholm WIT: Nielsen, Bettina Bryde WIT: Larsen, Ingrid Kjoller FERENCE: THOGERSEN =1 APPLICATION NUMBER: US/09/44 FELING DATE: 1998-06-11 PELICATION NUMBER: DK 0685/97 ILING DATE: 1998-06-11 PELICATION NUMBER: DK 0685/97 ILING DATE: 1998-06-11 PELICATION NUMBER: DK 0685/97 ILING DATE: 1997-06-11 PERSON ID NOS: 60 S: Patentin Ver. 2.0 S: 35
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7 8 9 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	RESULT 1 US-09-445-576-35 Sequence 35, Application US/(GENERAL INFORMATION: APPLICANT: Etzerodt, Michae APPLICANT: Graversen, Hans C APPLICANT: Graversen, Hans C APPLICANT: Holtet, Thor Las APPLICANT: Assrup, Jete 8 APPLICANT: Assrup, Jete 8 APPLICANT: Nielsen, Bettine APPLICANT: Larsen, Ingild K TITLE OF INVENTON: Larmeris FILE REFERENCE: THOGERSEN = 1 CURRENT PRILING DATE: 2000-(PRIOR FILING DATE: 1998-06-1 PRIOR FILING DATE: 1998-06-1 PRIOR FILING DATE: 1999-06-1 PRIOR FILING DATE: 1999-06-1 NUMBER OF SEQ ID NOS: 60 SOFTWARE: PALENTIN VET. 2.0 SSOFTWARE: PALENTIN VET. 2.0
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Gaps

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Indels

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0; Mismatches

Conservative

36;

Matches

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; OTHER INFORMATION: Description of Artificial Sequence:H6FXTN23
US-09-445-576-27
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APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Jobert, Severin
APPLICANT: Glordano, Jean-Yves
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.051.PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 172; DB 27;
Pred. No. 3.5e-15;
Mismatches 0;
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100.0%; Pred. No. 7.9e-15;
iive 0; Mismatches 0;
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APPLICANT: Etzercdt, Michael,
APPLICANT: Graversen, Niels Jonas Heilskov
APPLICANT: Kastrup, Jette Sandholm
APPLICANT: Kastrup, Jette Sandholm
APPLICANT: Kastrup, Jette Sandholm
APPLICANT: Mielsen, Bettina Bryde
APPLICANT: Larsen, Ingrid Kjoller
TITLE OF INVENTION: Trimerising module
FILE REFERENCE: THOGRESEN = 1
CURRENT APPLICATION NUMBER: US/09/445,576
CURRENT FILING DATE: 1998-06-07-17
PRIOR APPLICATION NUMBER: DCT/DX98/00245
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
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GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
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100.0%;
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Best Local Similarity 100.
Matches 36; Conservative
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Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: SIGNAL
; LOCATION: -21...1
US-60-197-873-13425
                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 13425
LENGTH: 95
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LENGTH: 180
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APPLICANT: Tanaka, Hiroaki,
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Johner, Severin
APPLICANT: Glordano, Jean-Yves
TITILE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 81.USZ-REG
CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT FILING DATE: 2001-04-13
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: PALENT.PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Pred. No. 1e-15;
0; Mismatches 0;
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1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
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GENERAL INFORMATION:
APPLICANT: GENERRES, Jonas
APPLICANT: MOESTRUP, Soren
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/987,107
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PATENT VERSION 3.1
SSOFTWARE: PATENT VERSION 3.1
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1 Similarity 100.0%; Pred. No. 1
36; Conservative 0; Mismatche
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US-09-987-107-39
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Matches 36; Conserv
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Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: SIGNAL
; LOCATION: -21. -1
US-09-834-366-13425
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APPLICANT: Bionomix, Inc.
APPLICANT: Debc, Derek
APPLICANT: Debc, Derek
APPLICANT: Debc, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILLE REPERBUCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN version 3.0
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RESULT 9

Sequence 62, Application US/09924340

Sequence 62, Application US/09924340

GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane

APPLICANT: Bejanin, Stephane

APPLICANT: Tanaka, Hiroaki

TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91 US2.REG

CURRENT APPLICATION NUMBER: US/09/924,340

CURRENT FILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: US 60/302,277

PRIOR PILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-06-19

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR PLICATION NUMBER: US 60/293,574

PRIOR APPLICATION NUMBER: US 60/293,574
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Pred. No. 9.2e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 172;
                             Sequence 41342, Application US/09791537 GENERAL INFORMATION:
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illarity 100.0%;
Conservative 0
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 36; Conserv
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       -09-791-537-41342.
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US-09-924-340-62
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US-09-445-576-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 197;
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100.0%; Pred. No. 8e-15;
iive 0; Mismatches 0;
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100.0%; Score 172; DB 18;
Best Local Similarity 100.0%; Pred. No. 8.9e-15;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/09445576
GENERAL INFORMATION:
APPLICANT: Thegersen, Hans Christian
APPLICANT: Etzerodt, Michael
APPLICANT: Etzerodt, Michael
APPLICANT: Gaversen, Nelso
APPLICANT: Gaversen, Nelso
APPLICANT: Gaversen, Nelso
APPLICANT: Mielsen, Bettina Bryde
APPLICANT: Mielsen, Bettina Bryde
APPLICANT: Instan, Bettina Bryde
APPLICANT: Instan, Bettina Bryde
APPLICANT: Instan, Bettina Bryde
APPLICANT: Mielsen, Bettina Bryde
APPLICANT: Mielsen, Bettina Bryde
TTILE OF INVENTION: Trimerising module
FILE REFERENCE: THOCERSEN -1
CURRENT FILING DATE: 2000-0-17
PRIOR APPLICATION NUMBER: PCT/PK98/00245
PRIOR APPLICATION NUMBER: PCT/PK98/00245
PRIOR APPLICATION NUMBER: DCT/PK98/00245
PRIOR APPLICATION NUMBER: DCT/PK98/00245
NUMBER OF SEQ ID NOS: 60
SEQ ID NO 25
LENGTH: 197
                                                            APPLICANT: LICETORIC, MICHOEL
APPLICANT: ELZEROGUC, MICHOEL
APPLICANT: Graversen, Niels Jonas Heilskov
APPLICANT: Graversen, Niels Jonas Heilskov
APPLICANT: Mastrup, Jette Sandholm
APPLICANT: Nielsen, Bettina Bryde
APPLICANT: Larsen, Ingrid Kjoller
TITLE OF INVENTION: Trimerising module
FILE REFERENCE: THOGERSEN =1
CURRENT FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: PCT/DK98/00245
PRIOR APPLICATION NUMBER: PCT/DK98/00245
PRIOR APPLICATION NUMBER: PCT/DK98/00245
PRIOR FILING DATE: 1997-06-11
PRIOR FILING DATE: 1997-06-11
SEO ID NO 7
LENGTHARE: PATENTIN Ver. 2.0
SEO ID NO 7
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Sequence 7, Application US/09445576
GENERAL INFORMATION:
APPLICANT: Thogersen, Hans Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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APPLICANT: Benjanin, Stephane

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Query Match 100.
Best Local Similarity 100.
Matches 36; Conservative
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ORGANISM: Homo sapiens
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; LOCATION: 1..21
US-10-000-489-62
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APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/992,600A
CURRENT FILING DATE: 2001-11-13
PRIOR PRILING DATE: 2001-11-13
PRIOR PLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR PLICATION NUMBER: PCT/IB01/01715
PRIOR PLICATION NUMBER: US 60/305,456
PRIOR PLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-19
PRIOR PLICATION NUMBER: US 60/298,698
PRIOR PLICATION NUMBER: US 60/298,698
PRIOR PLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
SOFTWARE: JPALENT
SOFTWARE: JPALENT
SOFTWARE: JPALENT
WANDER OF SEQ ID NOS: 114
SEQ ID NO 62
WANDER DATE
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APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 31.053.DIV
CURRENT FILING DATE: 2001-11-13
FRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-13
PRIOR PLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-15
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Best Local Similarity 100.0%; Pred. No. 9.2e-15;
Matches 36; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 9.2e-15;
ive 0; Mismatches 0;
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 36; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: SIGNAL
; LOCATION: 1. 21
US-09-992-600A-62
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APPLICANT: Tanaka, HITCAAKI
APPLICANT: Tanaka, HITCAAKI
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REBERBENCE: 91.056.DIV
CURRENT APPLICATION NUMBER: US/10/000,489
CURRENT FILING DATE: 2001-11-14
PRIOR PAPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-25
PRIOR PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
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PRIOR PRIOR FILING DATE: 2001-06-25
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GENERAL INFORMATION:
APPLICANT: Benjain, Stephane
APPLICANT: Tanaka, Hiroaki
ITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.039.DTV
CURRENT APPLICATION UNBER: US/10/000,986
CURRENT FILING DATE: 2001-11.14
FRIOR APPLICATION NUMBER: US 09/924,340
PRIOR PILING DATE: 2001-08-06
PRIOR PLING DATE: 2001-08-06
PRIOR PLING DATE: 2001-08-06
PRIOR PLING DATE: 2001-07-13
PRIOR PLING DATE: 2001-07-13
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-25
PRIOR PPLICATION NUMBER: US 60/293,574
PRIOR PPLING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 112
SOFTWARRE: JPRACENT
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1 VVNTKMFEELKSRLDTLAQEVALLKEQQALQTVCLK 36
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GENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
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                                                                                                                              Query Match 100.0%; Score 172; DB 24; Best Local Similarity 100.0%; Pred. No. 9.2e-15; Matches 36; Conservative 0; Mismatches 0;
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illarity 100.0%; Pred. No. 9.2e-15;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                           Sequence 62, Application US/60305456; GENERAL INFORMATION:
APPLICANT: BEJANIN, Stephane
APPLICANT: BEJANIN, Stephane
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS
FILE REFERENCE: 97.USS.PRO
CURRENT APPLICATION NUMBER: US/60/305,456
CURRENT FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 96
SOFTWARE PASSEQ for Windows Version 4.0
SEQ ID NO 62
LENGTH: 202
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CURRENT APPLICATION NUMBER: US/60/365,384
CURRENT FILING DATE: 2002-03-14
NUMBER OF SEQ ID NOS: 666
SOFTWARE: Pt_Genes Version 6.0
SEQ ID NO 579
LENGTH: 202
TYPE: PRT
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APPLICANT: Tang, Y. Tom
APPLICANT: Wang, Jian-rui
APPLICANT: Wang, Zhiwei
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Zhou, Ping
Wehrman, Tom
Wang, Jian-Rui
Ghosh, Malabika
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Xue, Aidong J.
Ma, Yunqing
Wang, Dunrui
Weng, Gezhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao, Qing A.
Asundi, Vinod
            TYPE: PRT
ORGANISM: Homo sapiens
FATURE:
NAME/KEY: SIGNAL
LOCATION: 1..21
US-10-000-986-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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Matches 36; Conserv
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LENGTH: 202
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APPLICANT:
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APPLICANT:
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